

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: MAERTENS, GEERT  
BOSMAN, FONS  
DE MARTYNOFF, GUY  
BUYSE, MARIE-ANGE

(ii) TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE  
PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE

(iii) NUMBER OF SEQUENCES: 111

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: NIXON & VANDERHYE P.C.  
(B) STREET: 1100 NORTH GLEBE ROAD  
(C) CITY: ARLINGTON  
(D) STATE: VIRGINIA  
(E) COUNTRY: U.S.A.  
(F) ZIP: 22201-4714

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/612,973  
(B) FILING DATE: 11-MAR-1996  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: BYRNE, THOMAS E.  
(B) REGISTRATION NUMBER: 32,205  
(C) REFERENCE/DOCKET NUMBER: 1487-10

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (703) 816-4000  
(B) TELEFAX: (703) 816-4100

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

09973025-101001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGCATGCAAG CTTAATTAAT T

21

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

CCGGGGAGGC CTGCACGTGA TCGAGGGCAG ACACCATCAC CACCATCACT AATAGTTAAT

60

FAACTGCA

68

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..639

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTA CTG TCC TGT  
Met Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys  
1 5 10 15

48

CTG ACC ATT CCA GCT TCC GCT TAT GAG GTG CGC AAC GTG TCC GGG ATG  
Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Met  
20 25 30

96

TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG TAT GAG GCA

144

Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala		
		35					40					45					
GCG	GAC	ATG	ATC	ATG	CAC	ACC	CCC	GGG	TGC	GTG	CCC	TGC	GTT	CGG	GAG	192	
Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu		
		50				55					60						
AAC	AAC	TCT	TCC	CGC	TGC	TGG	GTA	GCG	CTC	ACC	CCC	ACG	CTC	GCA	GCT	240	
Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala		
		65			70					75					80		
AGG	AAC	GCC	AGC	GTC	CCC	ACC	ACG	ACA	ATA	CGA	CGC	CAC	GTC	GAT	TTG	288	
Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	Val	Asp	Leu		
				85					90					95			
CTC	GTT	GGG	GCG	GCT	GCT	CTC	TGT	TCC	GCT	ATG	TAC	GTG	GGG	GAT	CTC	336	
Leu	Val	Gly	Ala	Ala	Leu	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu			
			100					105					110				
TGC	GGA	TCT	GTC	TTC	CTC	GTC	TCC	CAG	CTG	TTC	ACC	ATC	TCG	CCT	CGC	384	
Cys	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Ile	Ser	Pro	Arg		
			115				120					125					
CGG	CAT	GAG	ACG	GTG	CAG	GAC	TGC	AAT	TGC	TCA	ATC	TAT	CCC	GGC	CAC	432	
Arg	His	Glu	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	His		
		130				135					140						
ATA	ACA	GGT	CAC	CGT	ATG	GCT	TGG	GAT	ATG	ATG	ATG	AAC	TGG	TCG	CCT	480	
Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	Ser	Pro		
					150					155					160		
ACA	ACG	GCC	CTG	GTG	GTA	TCG	CAG	CTG	CTC	CGG	ATC	CCA	CAA	GCT	GTC	528	
Thr	Thr	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro	Gln	Ala	Val		
				165					170					175			
GTG	GAC	ATG	GTG	GCG	GGG	GCC	CAT	TGG	GGA	GTC	CTG	GCG	GGC	CTC	GCC	576	
Val	Asp	Met	Val	Ala	Gly	Ala	His	Trp	Gly	Val	Leu	Ala	Gly	Leu	Ala		
			180					185					190				
TAC	TAT	TCC	ATG	GTG	GGG	AAC	TGG	GCT	AAG	GTT	TTG	ATT	GTG	ATG	CTA	624	
Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val	Leu	Ile	Val	Met	Leu		
		195					200					205					
CTC	TTT	GCT	CTC	TAATAG												642	
Leu	Phe	Ala	Leu														
			210														

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 212 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys
1				5				10						15	

Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Met  
                     20                    25                    30  
 Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala  
                     35                    40                    45  
 Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu  
                     50                    55                    60  
 Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala  
                     65                    70                    75                    80  
 Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu  
                     85                    90                    95  
 Leu Val Gly Ala Ala Ala Leu Cys Ser Ala Met Tyr Val Gly Asp Leu  
                     100                    105                    110  
 Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile Ser Pro Arg  
                     115                    120                    125  
 Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His  
                     130                    135                    140  
 Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser Pro  
                     145                    150                    155                    160  
 Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro Gln Ala Val  
                     165                    170                    175  
 Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala  
                     180                    185                    190  
 Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Ile Val Met Leu  
                     195                    200                    205  
 Leu Phe Ala Leu  
                     210

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 795 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..792

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide  
(B) LOCATION: 1..789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC	48
Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	
GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG	96
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20 25 30	
GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA	144
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35 40 45	
ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG	192
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
50 55 60	
CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG	240
Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	
65 70 75 80	
TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG	288
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	
85 90 95	
TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC	336
Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys	
100 105 110	
GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG	384
Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr	
115 120 125	
CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC	432
Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His	
130 135 140	
GTC GAT TTG CTC GTT GGG GCG GCT GCT TTC TGT TCC GCT ATG TAC GTG	480
Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val	
145 150 155 160	
GGG GAC CTC TGC GGA TCT GTC TTC CTC GTC TCC CAG CTG TTC ACC ATC	528
Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile	
165 170 175	
TCG CCT CGC CGG CAT GAG ACG GTG CAG GAC TGC AAT TGC TCA ATC TAT	576
Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr	
180 185 190	
CCC GGC CAC ATA ACG GGT CAC CGT ATG GCT TGG GAT ATG ATG ATG AAC	624
Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn	
195 200 205	
TGG TCG CCT ACA ACG GCC CTG GTG GTA TCG CAG CTG CTC CGG ATC CCA	672
Trp Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro	
210 215 220	

CAA GCT GTC GTG GAC ATG GTG GCG GGG GCC CAT TGG GGA GTC CTG GCG	720
Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala	
225 230 235 240	
GGT CTC GCC TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG ATT	768
Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Ile	
245 250 255	
GTG ATG CTA CTC TTT GCT CCC TAATAG	795
Val Met Leu Leu Phe Ala Pro	
260	

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu  
1 5 10 15

Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg  
20 25 30

Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala  
35 40 45

Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu  
50 55 60

Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val  
65 70 75 80

Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val  
85 90 95

Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys  
100 105 110

Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr  
115 120 125

Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His  
130 135 140

Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val  
145 150 155 160

Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile  
165 170 175

Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr  
180 185 190

Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn  
195 200 205

Trp Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro  
210 215 220

Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala  
225 230 235 240

Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Ile  
245 250 255

Val Met Leu Leu Phe Ala Pro  
260

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..630

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..627

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ATG TTG GGT AAG GTC ATC GAT ACC CTT ACG TGC GGC TTC GCC GAC CTC	48
Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	
ATG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGT GCT GCC AGA	96
Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20 25 30	
GCC CTG GCG CAT GGC GTC CGG GTT CTG GAA GAC GGC GTG AAC TAT GCA	144
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35 40 45	
ACA GGG AAT TTG CCT GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTA	192
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
50 55 60	
CTG TCC TGT CTG ACC ATT CCA GCT TCC GCT TAT GAG GTG CGC AAC GTG	240
Leu Ser Cys Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	
65 70 75 80	

TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG	288
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	
85 90 95	
TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC	336
Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys	
100 105 110	
GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG	384
Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr	
115 120 125	
CTC GCA GCT AGG AAC GCC AGC GTC CCC ACT ACG ACA ATA CGA CGC CAC	432
Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His	
130 135 140	
GTC GAT TTG CTC GTT GGG GCG GCT GCT TTC TGT TCC GCT ATG TAC GTG	480
Val Asp Leu Leu Val Gly Ala Ala Phe Cys Ser Ala Met Tyr Val	
145 150 155 160	
GGG GAT CTC TGC GGA TCT GTC TTC CTC GTC TCC CAG CTG TTC ACC ATC	528
Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile	
165 170 175	
TCG CCT CGC CGG CAT GAG ACG GTG CAG GAC TGC AAT TGC TCA ATC TAT	576
Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr	
180 185 190	
CCC GGC CAC ATA ACA GGT CAC CGT ATG GCT TGG GAT ATG ATG ATG AAC	624
Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn	
195 200 205	
TGG TAATAG	633
Trp	
210	

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu
1 5 10 15
Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg
20 25 30
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala
35 40 45
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu
50 55 60





Leu	Thr	Ile	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Val		
			20					25					30				
TAC	CAT	GTC	ACG	AAC	GAC	TGC	TCC	AAC	TCA	AGC	ATA	GTG	TAT	GAG	GCA	144	
Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala		
		35					40					45					
GCG	GAC	ATG	ATC	ATG	CAC	ACC	CCC	GGG	TGC	GTG	CCC	TGC	GTT	CGG	GAG	192	
Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu		
		50				55					60						
GGC	AAC	TCC	TCC	CGT	TGC	TGG	GTG	GCG	CTC	ACT	CCC	ACG	CTC	GCG	GCC	240	
Gly	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala		
	65				70				75					80			
AGG	AAC	GCC	AGC	GTC	CCC	ACA	ACG	ACA	ATA	CGA	CGC	CAC	GTC	GAT	TTG	288	
Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	Val	Asp	Leu		
				85					90					95			
CTC	GTT	GGG	GCT	GCT	GCT	TTC	TGT	TCC	GCT	ATG	TAC	GTG	GGG	GAT	CTC	336	
Leu	Val	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu		
			100					105					110				
TGC	GGA	TCT	GTT	TTC	CTT	GTT	TCC	CAG	CTG	TTC	ACC	TTC	TCA	CCT	CGC	384	
Cys	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg		
		115					120					125					
CGG	CAT	CAA	ACA	GTA	CAG	GAC	TGC	AAC	TGC	TCA	ATC	TAT	CCC	GGC	CAT	432	
Arg	His	Gln	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	His		
		130				135					140						
GTA	TCA	GGT	CAC	CGC	ATG	GCT	TGG	GAT	ATG	ATG	ATG	AAC	TGG	TCC	TAATAG	483	
Val	Ser	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	Ser			
		145			150				155					160			

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys		
1				5					10					15			
Leu	Thr	Ile	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Val		
			20					25					30				
Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala		
		35					40					45					
Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu		
		50				55					60						
Gly	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala		
	65				70				75					80			

Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu  
85 90 95  
Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu  
100 105 110  
Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg  
115 120 125  
Arg His Gln Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His  
130 135 140  
Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser  
145 150 155

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..477

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ATG TCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCC CTG CTG TCC TGT	48
Met Ser Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys	
1 5 10 15	
CTG ACC ATA CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG TCC GGG GTG	96
Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Val	
20 25 30	
TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATA GTG TAT GAG GCA	144
Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala	
35 40 45	
GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT CGG GAG	192
Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu	
50 55 60	
GGC AAC TCC TCC CGT TGC TGG GTG GCG CTC ACT CCC ACG CTC GCG GCC	240
Gly Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala	
65 70 75 80	

AGG AAC GCC AGC GTC CCC ACA ACG ACA ATA CGA CGC CAC GTC GAT TTG	288
Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu	
85 90 95	
CTC GTT GGG GCT GCT GCT TTC TGT TCC GCT ATG TAC GTG GGG GAT CTC	336
Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu	
100 105 110	
TGC GGA TCT GTT TTC CTT GTT TCC CAG CTG TTC ACC TTC TCA CCT CGC	384
Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg	
115 120 125	
CGG CAT CAA ACA GTA CAG GAC TGC AAC TGC TCA ATC TAT CCC GGC CAT	432
Arg His Gln Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His	
130 135 140	
GTA TCA GGT CAC CGC ATG GCT TGG GAT ATG ATG ATG AAC TGG TAATAG	480
Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp	
145 150 155	

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 158 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met	Ser	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys	1	5	10	15
Leu	Thr	Ile	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Val	20	25	30	
Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	35	40	45	
Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	50	55	60	
Gly	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	65	70	75	80
Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	Val	Asp	Leu	85	90	95	
Leu	Val	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu	100	105	110	
Cys	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg	115	120	125	
Arg	His	Gln	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	His	130	135	140	
Val	Ser	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp			145	150	155	

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..633

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

09973022510011001200130014001500160017001800190020002100220023002400250026002700280029003000310032003300340035003600370038003900400041004200430044004500460047004800490050005100520053005400550056005700580059006000610062006300640065006600670068006900700071007200730074007500760077007800790080008100820083008400850086008700880089009000910092009300940095009600970098009900100010100102001030010400105001060010700108001090011001110011200113001140011500116001170011800119001200121001220012300124001250012600127001280012900130013100132001330013400135001360013700138001390014001410014200143001440014500146001470014800149001500151001520015300154001550015600157001580015900160016100162001630016400165001660016700168001690017001710017200173001740017500176001770017800179001800181001820018300184001850018600187001880018900190019100192001930019400195001960019700198001990020002010020200203002040020500206002070020800209002100211002120021300214002150021600217002180021900220022100222002230022400225002260022700228002290023002310023200233002340023500236002370023800239002400241002420024300244002450024600247002480024900250025100252002530025400255002560025700258002590026002610026200263002640026500266002670026800269002700271002720027300274002750027600277002780027900280028100282002830028400285002860028700288002890029002910029200293002940029500296002970029800299003000301003020030300304003050030600307003080030900310031100312003130031400315003160031700318003190032003210032200323003240032500326003270032800329003300331003320033300334003350033600337003380033900340034100342003430034400345003460034700348003490035003510035200353003540035500356003570035800359003600361003620036300364003650036600367003680036900370037100372003730037400375003760037700378003790038003810038200383003840038500386003870038800389003900391003920039300394003950039600397003980039900400040100402004030040400405004060040700408004090041004110041200413004140041500416004170041800419004200421004220042300424004250042600427004280042900430043100432004330043400435004360043700438004390044004410044200443004440044500446004470044800449004500451004520045300454004550045600457004580045900460046100462004630046400465004660046700468004690047004710047200473004740047500476004770047800479004800481004820048300484004850048600487004880048900490049100492004930049400495004960049700498004990050005010050200503005040050500506005070050800509005100511005120051300514005150051600517005180051900520052100522005230052400525005260052700528005290053005310053200533005340053500536005370053800539005400541005420054300544005450054600547005480054900550055100552005530055400555005560055700558005590056005610056200563005640056500566005670056800569005700571005720057300574005750057600577005780057900580058100582005830058400585005860058700588005890059005910059200593005940059500596005970059800599006000601006020060300604006050060600607006080060900610061100612006130061400615006160061700618006190062006210062200623006240062500626006270062800629006300631006320063300634006350063600637006380063900640064100642006430064400645006460064700648006490065006510065200653006540065500656006570065800659006600661006620066300664006650066600667006680066900670067100672006730067400675006760067700678006790068006810068200683006840068500686006870068800689006900691006920069300694006950069600697006980069900700070100702007030070400705007060070700708007090071007110071200713007140071500716007170071800719007200721007220072300724007250072600727007280072900730073100732007330073400735007360073700738007390074007410074200743007440074500746007470074800749007500751007520075300754007550075600757007580075900760076100762007630076400765007660076700768007690077007710077200773007740077500776007770077800779007800781007820078300784007850078600787007880078900790079100792007930079400795007960079700798007990080008010080200803008040080500806008070080800809008100811008120081300814008150081600817008180081900820082100822008230082400825008260082700828008290083008310083200833008340083500836008370083800839008400841008420084300844008450084600847008480084900850085100852008530085400855008560085700858008590086008610086200863008640086500866008670086800869008700871008720087300874008750087600877008780087900880088100882008830088400885008860088700888008890089008910089200893008940089500896008970089800899009000901009020090300904009050090600907009080090900910091100912009130091400915009160091700918009190092009210092200923009240092500926009270092800929009300931009320093300934009350093600937009380093900940094100942009430094400945009460094700948009490095009510095200953009540095500956009570095800959009600961009620096300964009650096600967009680096900970097100972009730097400975009760097700978009790098009810098200983009840098500986009870098800989009900991009920099300994009950099600997009980099901000100101001011010120101301014010150101601017010180101901020102101022010230102401025010260102701028010290103010310103201033010340103501036010370103801039010401041010420104301044010450104601047010480104901050105101052010530105401055010560105701058010590106010610106201063010640106501066010670106801069010701071010720107301074010750107601077010780107901080108101082010830108401085010860108701088010890109010910109201093010940109501096010970109801099011001101011020110301104011050110601107011080110901110111101112011130111401115011160111701118011190112011210112201123011240112501126011270112801129011301131011320113301134011350113601137011380113901140114101142011430114401145011460114701148011490115011510115201153011540115501156011570115801159011601161011620116301164011650116601167011680116901170117101172011730117401175011760117701178011790118011810118201183011840118501186011870118801189011901191011920119301194011950119601197011980119901200120101202012030120401205012060120701208012090121012110121201213012140121501216012170121801219012201221012220122301224012250122601227012280122901230123101232012330123401235012360123701238012390124012410124201243012440124501246012470124801249012501251012520125301254012550125601257012580125901260126101262012630126401265012660126701268012690127012710127201273012740127501276012770127801279012801281012820128301284012850128601287012880128901290129101292012930129401295012960129701298012990130013010130201303013040130501306013070130801309013101311013120131301314013150131601317013180131901320132101322013230132401325013260132701328013290133013310133201333013340133501336013370133801339013401341013420134301344013450134601347013480134901350135101352013530135401355013560135701358013590136013610136201363013640136501366013670136801369013701371013720137301374013750137601377013780137901380138101382013830138401385013860138701388013890139013910139201393013940139501396013970139801399014001401014020140301404014050140601407014080140901410141101412014130141401415014160141701418014190142014210142201423014240142501426014270142801429014301431014320143301434014350143601437014380143901440144101442014430144401445014460144701448014490145014510145201453014540145501456014570145801459014601461014620146301464014650146601467014680146901470147101472014730147401475014760147701478014790148014810148201483014840148501486014870148801489014901491014920149301494014950149601497014980149901500150101502015030150401505015060150701508015090151015110151201513015140151501516015170151801519015201521015220152301524015250152601527015280152901530153101532015330153401535015360153701538015390154015410154201543015440154501546015470154801549015501551015520155301554015550155601557015580155901560156101562015630156401565015660156701568015690157015710157201573015740157501576015770157801579015801581015820158301584015850158601587015880158901590159101592015930159401595015960159701598015990160016010160201603016040160501606016070160801609016101611016120161301614016150161601617016180161901620162101622016230162401625016260162701628016290163016310163201633016340163501636016370163801639016401641016420164301644016450164601647016480164901650165101652016530165401655016560165701658016590166016610166201663016640166501666016670166801669016701671016720167301674016750167601677016780167901680168101682016830168401685016860168701688016890169016910169201693016940169501696016970169801699017001701017020170301704017050170601707017080170901710171101712017130171401715017160171701718017190172017210172201723017240172501726017270172801729017301731017320173301734017350173601737017380173901740174101742017430174401745017460174701748017490175017510175201753017540175501756017570175801759017601761017620176301764017650176601767017680176901770177101772017730177401775017760177701778017790178017810178201783017840178501786017870178801789017901791017920179301794017950179601797017980179901800180101802018030180401805018060180701808018090181018110181201813018140181501816018170181801819018201821018220182301824018250182601827018280182901830183101832018330183401835018360183701838018390184018410184201843018440184501846018470184801849018501851018520185301854018550185601857018580185901860186101862018630186401865018660186701868018690187018710187201873018740187501876018770187801879018801881018820188301884018850188601887018880188901890189101892018930189401895018960189701898018990190019010190201903019040190501906019070190801909019101911019120191301914019150191601917019180191901920192101922019230192401925019260192701928019290193019310193201933019340193501936019370193801939019401941019420194301944019450194601947019480194901950195101952019530195401955019560195701958019590196019610196201963019640196501966019670196801969019701971019720197301974019750197601977019780197901980198101982019830198401985019860198701988019890199019910199201993019940199501996019970199801999020002001020020200302004020050200602007020080200902010201102012020130201402015020160201702018020190202020210202202023020240202502026020270202802029020302031020320203302034020350203602037020380203902040204102042020430204402045020460204702048020490205020510205202053020540205502056020570205802059020602061020620206302064020650206602067020680206902070207102072020730207402075020760207702078020790208020810208202083020840208502086020870208802089020902091020920209302094020950209602097020980209902100210102102021030210402105021060210702108021090211021110211202113021140211502116021170211802119021202121021220212302124021250212602127021280212902130213102132021330213402135021360213702138021390214021410214202143021440214502146021470214802149021502151021520215302154021550215602157021580215902160216102162021630216402165021660216702168021690217021710217202173021740217502176021770217802179021802181021820218302184021850218602187021880218902190219102192021930219402195021960219702198021990220022010220202203022040220502206022070220802209022102211022120221302214022150221602217022180221902220222102222022230222402225022260222702228022290223022310223202233022340223502236022370223802239022402241022420224302244022450224602247022480224902250225102252022530225402255022560225702258022590226022610226202263022640226502266022670226802269022702271022720227302274022750227602277022780227902280228102282022830228402285022860228702288022890229022910229202293022940229502296022970229802299023002301023020230302304023050230602307023080230902310231102312023130231402315023160231702318023190232023210232202323023240232502326023270232802329023302331023320233302334023350233602337023380233902340234102342023430234402345023460234702348023490235023510235202353023540235502356023570235802359023602361023620236302364023650236602367023680236902370237102372023730237402375023760237702378023790238023810238202383023840238502386023870238802389023902391023920239302394023950239602397023980239902400240102402024030240402405024060240702408024090241024110241202413024140241502416024170241802419024202421024220242302424024250242602427024280242902430243102432024330243402435024360243702438024390244

Leu Ala Ala Arg Asn Ala Ser Ile Pro Thr Thr Thr Ile Arg Arg His  
 130 135 140

GTC GAT TTG CTC GTT GGG GCG GCT GCT TTC TGT TCC GCT ATG TAC GTG 480  
 Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val  
 145 150 155 160

GGG GAT CTC TGC GGA TCT GTC TTC CTC GTC TCC CAG CTG TTC ACC ATC 528  
 Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile  
 165 170 175

TCG CCT CGC CGG CAT GAG ACG GTG CAG GAC TGC AAT TGC TCA ATC TAT 576  
 Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr  
 180 185 190

CCC GGC CAC ATA ACG GGT CAC CGT ATG GCT TGG GAT ATG ATG ATG AAC 624  
 Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn  
 195 200 205

TGG TAC TAATAG 640  
 Trp Tyr  
 210

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met Leu Gly Lys Ala Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu  
 1 5 10 15

Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg  
 20 25 30

Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala  
 35 40 45

Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu  
 50 55 60

Leu Ser Cys Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val  
 65 70 75 80

Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val  
 85 90 95

Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys  
 100 105 110

Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr  
 115 120 125

Leu Ala Ala Arg Asn Ala Ser Ile Pro Thr Thr Thr Ile Arg Arg His

130	135	140
Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val		
145	150	155 160
Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile		
	165	170 175
Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr		
	180	185 190
Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn		
	195	200 205
Trp Tyr		
210		

69973025-101001

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

ATGCCCGGTT GCTCTTCTC TATCTT

26

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

ATGTTGGGTA AGGTCATCGA TACCCT

26

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CTATTAGGAC CAGTTCATCA TCATATCCCA

30

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

CTATTACCAG TTCATCATCA TATCCCA

27

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

ATACGACGCC ACGTCGATTC CCAGCTGTTC ACCATC

36

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs



- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GATGGTGAAC AGCTGGGAAT CGACGTGGCG TCGTAT

36

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..720

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC	48
Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	
GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG	96
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20 25 30	
GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA	144
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35 40 45	
ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG	192
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
50 55 60	
CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG	240
Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	
65 70 75 80	

TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG	288
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	
85 90 95	
TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC	336
Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys	
100 105 110	
GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG	384
Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr	
115 120 125	
CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC	432
Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His	
130 135 140	
GTC GAT TCC CAG CTG TTC ACC ATC TCG CCT CGC CGG CAT GAG ACG GTG	480
Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val	
145 150 155 160	
CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC ATA ACG GGT CAC CGT	528
Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg	
165 170 175	
ATG GCT TGG GAT ATG ATG ATG AAC TGG TCG CCT ACA ACG GCC CTG GTG	576
Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val	
180 185 190	
GTA TCG CAG CTG CTC CGG ATC CCA CAA GCT GTC GTG GAC ATG GTG GCG	624
Val Ser Gln Leu Leu Arg Ile Pro Gln Ala Val Val Asp Met Val Ala	
195 200 205	
GGG GCC CAT TGG GGA GTC CTG GCG GGT CTC GCC TAC TAT TCC ATG GTG	672
Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val	
210 215 220	
GGG AAC TGG GCT AAG GTT TTG ATT GTG ATG CTA CTC TTT GCT CCC TAATAG	723
Gly Asn Trp Ala Lys Val Leu Ile Val Met Leu Leu Phe Ala Pro	
225 230 235 240	

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20 25 30	
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35 40 45	

Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu
	50					55					60				
Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val
65					70					75					80
Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val
				85					90					95	
Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys
			100					105					110		
Val	Arg	Glu	Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr
		115					120					125			
Leu	Ala	Ala	Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His
		130					135					140			
Val	Asp	Ser	Gln	Leu	Phe	Thr	Ile	Ser	Pro	Arg	Arg	His	Glu	Thr	Val
145					150					155					160
Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	His	Ile	Thr	Gly	His	Arg
			165						170					175	
Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	Ser	Pro	Thr	Thr	Ala	Leu	Val
			180					185					190		
Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro	Gln	Ala	Val	Val	Asp	Met	Val	Ala
		195					200					205			
Gly	Ala	His	Trp	Gly	Val	Leu	Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Val
	210					215					220				
Gly	Asn	Trp	Ala	Lys	Val	Leu	Ile	Val	Met	Leu	Leu	Phe	Ala	Pro	
225					230					235					

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 561 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..558

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC	48
Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	
GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG	96
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20 25 30	
GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA	144
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35 40 45	
ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG	192
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
50 55 60	
CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG	240
Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	
65 70 75 80	
TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG	288
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	
85 90 95	
TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC	336
Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys	
100 105 110	
GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG	384
Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr	
115 120 125	
GTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC	432
Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His	
130 135 140	
GTC GAT TCC CAG CTG TTC ACC ATC TCG CCT CGC CGG CAT GAG ACG GTG	480
Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val	
145 150 155 160	
CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC ATA ACG GGT CAC CGT	528
Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg	
165 170 175	
ATG GCT TGG GAT ATG ATG ATG AAC TGG TAATAG	561
Met Ala Trp Asp Met Met Met Asn Trp	
180 185	

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu

1	5	10	15
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	20	25	30
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	35	40	45
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	50	55	60
Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	65	70	75
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	85	90	95
Thr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys	100	105	110
Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr	115	120	125
Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His	130	135	140
Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val	145	150	155
Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg	165	170	175
Met Ala Trp Asp Met Met Met Asn Trp	180	185	

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 606 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..603

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC	48
Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	
GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG	96
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20 25 30	
GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA	144
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35 40 45	
ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG	192
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
50 55 60	
CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG	240
Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	
65 70 75 80	
TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG	288
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	
85 90 95	
TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC	336
Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys	
100 105 110	
GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG	384
Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr	
115 120 125	
GTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC	432
Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His	
130 135 140	
GTC GAT TCC CAG CTG TTC ACC ATC TCG CCT CGC CGG CAT GAG ACG GTG	480
Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val	
145 150 155 160	
CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC ATA ACG GGT CAC CGT	528
Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg	
165 170 175	
ATG GCT TGG GAT ATG ATG ATG AAC TGG TCG CCT ACA ACG GCC CTG GTG	576
Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val	
180 185 190	
GTA TCG CAG CTG CTC CGG ATC CTC TAATAG	606
Val Ser Gln Leu Leu Arg Ile Leu	
195 200	

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 200 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu  
1 5 10 15  
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg  
20 25 30  
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala  
35 40 45  
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu  
50 55 60  
Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val  
65 70 75 80  
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val  
85 90 95  
Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys  
100 105 110  
Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr  
115 120 125  
Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His  
130 135 140  
Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val  
145 150 155 160  
Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg  
165 170 175  
Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val  
180 185 190  
Val Ser Gln Leu Leu Arg Ile Leu  
195 200

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 636 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 1..633

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: 1..630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

ATG	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTT	ACA	TGC	GGC	TTC	GCC	GAC	CTC	48
Met	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu	
1				5				10						15		
GTG	GGG	TAC	ATT	CCG	CTC	GTC	GGC	GCC	CCC	CTA	GGG	GGC	GCT	GCC	AGG	96
Val	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg	
			20					25					30			
GCC	CTG	GCG	CAT	GGC	GTC	CGG	GTT	CTG	GAG	GAC	GGC	GTG	AAC	TAT	GCA	144
Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	
			35				40					45				
ACA	GGG	AAT	TTG	CCC	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTC	TTG	GCT	TTG	192
Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	
	50					55					60					
CTG	TCC	TGT	CTG	ACC	GTT	CCA	GCT	TCC	GCT	TAT	GAA	GTG	CGC	AAC	GTG	240
Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val	
65					70					75					80	
TCC	GGG	ATG	TAC	CAT	GTC	ACG	AAC	GAC	TGC	TCC	AAC	TCA	AGC	ATT	GTG	288
Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	
				85					90					95		
TAT	GAG	GCA	GCG	GAC	ATG	ATC	ATG	CAC	ACC	CCC	GGG	TGC	GTG	CCC	TGC	336
Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	
			100					105					110			
GTT	CGG	GAG	AAC	AAC	TCT	TCC	CGC	TGC	TGG	GTA	GCG	CTC	ACC	CCC	ACG	384
Val	Arg	Glu	Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	
			115				120					125				
CTC	GCA	GCT	AGG	AAC	GCC	AGC	GTC	CCC	ACC	ACG	ACA	ATA	CGA	CGC	CAC	432
Leu	Ala	Ala	Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	
			130				135					140				
GTC	GAT	TCC	CAG	CTG	TTC	ACC	ATC	TCG	CCT	CGC	CGG	CAT	GAG	ACG	GTG	480
Val	Asp	Ser	Gln	Leu	Phe	Thr	Ile	Ser	Pro	Arg	Arg	His	Glu	Thr	Val	
145					150					155					160	
CAG	GAC	TGC	AAT	TGC	TCA	ATC	TAT	CCC	GGC	CAC	ATA	ACG	GGT	CAC	CGT	528
Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	His	Ile	Thr	Gly	His	Arg	
				165					170					175		
ATG	GCT	TGG	GAT	ATG	ATG	ATG	AAC	TGG	TCG	CCT	ACA	ACG	GCC	CTG	GTG	576
Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	Ser	Pro	Thr	Thr	Ala	Leu	Val	
			180					185					190			
GTA	TCG	CAG	CTG	CTC	CGG	ATC	GTG	ATC	GAG	GGC	AGA	CAC	CAT	CAC	CAC	624
Val	Ser	Gln	Leu	Leu	Arg	Ile	Val	Ile	Glu	Gly	Arg	His	His	His	His	
			195				200					205				
CAT	CAC	TAATAG														636
His	His															



## (2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 210 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu  
 1 5 10 15  
 Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg  
 20 25 30  
 Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala  
 35 40 45  
 Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu  
 50 55 60  
 Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val  
 65 70 75 80  
 Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val  
 85 90 95  
 Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys  
 100 105 110  
 Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr  
 115 120 125  
 Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His  
 130 135 140  
 Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val  
 145 150 155 160  
 Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg  
 165 170 175  
 Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val  
 180 185 190  
 Val Ser Gln Leu Leu Arg Ile Val Ile Glu Gly Arg His His His His  
 195 200 205  
 His His  
 210

## (2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 630 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..627

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: 1..624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

09973  
Met 1  
GGG  
GTT  
Gly  
GGG  
Gly  
TCT  
Ser  
65  
GGC  
Gly  
GAG  
Gln  
GCA  
Ala  
130  
GAC  
Asp  
145

ATG GGT AAG GTC ATC GAT ACC CTT ACG TGC GGA TTC GCC GAT CTC ATG  
Met Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu Met  
5 10 15

GGG TAC ATC CCG CTC GTC GGC GCT CCC GTA GGA GGC GTC GCA AGA GCC  
Gly Tyr Ile Pro Leu Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala  
20 25 30

GTT GCG CAT GGC GTG AGG GCC CTT GAA GAC GGG ATA AAT TTC GCA ACA  
Leu Ala His Gly Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr  
35 40 45

GGG AAT TTG CCC GGT TGC TCC TTT TCT ATT TTC CTT CTC GCT CTG TTC  
Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe  
50 55 60

TCT TGC TTA ATT CAT CCA GCA GCT AGT CTA GAG TGG CGG AAT ACG TCT  
Ser Cys Leu Ile His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser  
65 70 75 80

GGC CTC TAT GTC CTT ACC AAC GAC TGT TCC AAT AGC AGT ATT GTG TAC  
Gly Leu Tyr Val Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr  
85 90 95

GAG GCC GAT GAC GTT ATT CTG CAC ACA CCC GGC TGC ATA CCT TGT GTC  
Glu Ala Asp Asp Val Ile Leu His Thr Pro Gly Cys Ile Pro Cys Val  
100 105 110

CAG GAC GGC AAT ACA TCC ACG TGC TGG ACC CCA GTG ACA CCT ACA GTG  
Gln Asp Gly Asn Thr Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val  
115 120 125

GCA GTC AAG TAC GTC GGA GCA ACC ACC GCT TCG ATA CGC AGT CAT GTG  
Ala Val Lys Tyr Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val  
130 135 140

GAC CTA TTA GTG GGC GCG GCC ACG ATG TGC TCT GCG CTC TAC GTG GGT  
Asp Leu Leu Val Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly  
145 150 155 160

48  
96  
144  
192  
240  
288  
336  
384  
432  
480



Pro Arg Arg His Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro  
180 185 190

Gly His Leu Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp  
195 200 205

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 630 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 1..627

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide  
(B) LOCATION: 1..624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

ATG GGT AAG GTC ATC GAT ACC CTA ACG TGC GGA TTC GCC GAT CTC ATG	48
Met Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu Met	
1 5 10 15	
GGG TAT ATC CCG CTC GTA GGC GGC CCC ATT GGG GGC GTC GCA AGG GCT	96
Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile Gly Gly Val Ala Arg Ala	
20 25 30	
CTC GCA CAC GGT GTG AGG GTC CTT GAG GAC GGG GTA AAC TAT GCA ACA	144
Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr	
35 40 45	
GGG AAT TTA CCC GGT TGC TCT TTC TCT ATC TTT ATT CTT GCT CTT CTC	192
Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Ile Leu Ala Leu Leu	
50 55 60	
TCG TGT CTG ACC GTT CCG GCC TCT GCA GTT CCC TAC CGA AAT GCC TCT	240
Ser Cys Leu Thr Val Pro Ala Ser Ala Val Pro Tyr Arg Asn Ala Ser	
65 70 75 80	
GGG ATT TAT CAT GTT ACC AAT GAT TGC CCA AAC TCT TCC ATA GTC TAT	288
Gly Ile Tyr His Val Thr Asn Asp Cys Pro Asn Ser Ser Ile Val Tyr	
85 90 95	
GAG GCA GAT AAC CTG ATC CTA CAC GCA CCT GGT TGC GTG CCT TGT GTC	336



Glu Ala Asp Asn Leu Ile Leu His Ala Pro Gly Cys Val Pro Cys Val  
 100 105 110  
 Met Thr Gly Asn Val Ser Arg Cys Trp Val Gln Ile Thr Pro Thr Leu  
 115 120 125  
 Ser Ala Pro Ser Leu Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val  
 130 135 140  
 Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly  
 145 150 155 160  
 Asp Ala Cys Gly Ala Leu Phe Leu Val Gly Gln Met Phe Thr Tyr Arg  
 165 170 175  
 Pro Arg Gln His Ala Thr Val Gln Asn Cys Asn Cys Ser Ile Tyr Ser  
 180 185 190  
 Gly His Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp  
 195 200 205

00973022-101001

(2) INFORMATION FOR SEQ ID NO: 33:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

TGGGATATGA TGATGAACTG GTC

23

(2) INFORMATION FOR SEQ ID NO: 34:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

30

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1476 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..1473

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(ix) FEATURE:
      (A) NAME/KEY: mat_peptide
      (B) LOCATION: 1..1470
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

PGG GAT ATG ATG ATG AAC TGG TCG CCT ACA ACG GCC CTG GTG GTA TCG 48  
 Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val Val Ser  
 1 5 10 15

CAG CTG CTC CGG ATC CCA CAA GCT GTC GTG GAC ATG GTG GCG GGG GCC 96  
 Gln Leu Leu Arg Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala  
 20 25 30

CAT TGG GGA GTC CTG GCG GGC CTC GCC TAC TAT TCC ATG GTG GGG AAC 144  
His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn  
35 40 45

TGG GCT AAG GTT TTG GTT GTG ATG CTA CTC TTT GCC GGC GTC GAC GGG 192  
Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly  
50 55 60

CAT ACC CGC GTG TCA GGA GGG GCA GCA GCC TCC GAT ACC AGG GGC CTT 240  
His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu  
65 70 75 80

GTG	TCC	CTC	TTT	AGC	CCC	GGG	TCG	GCT	CAG	AAA	ATC	CAG	CTC	GTA	AAC	288
Val	Ser	Leu	Phe	Ser	Pro	Gly	Ser	Ala	Gln	Lys	Ile	Gln	Leu	Val	Asn	
				85					90					95		

ACC AAC GGC AGT TGG CAC ATC AAC AGG ACT GCC CTG AAC TGC AAC GAC  
Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp 336

TCC CTC CAA ACA GGG TTC TTT GCC GCA CTA TTC TAC AAA CAC AAA TTC 384  
Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe  
115 120 125

AAC TCG TCT GGA TGC CCA GAG CGC TTG GCC AGC TGT CGC TCC ATC GAC 432

Asn	Ser	Ser	Gly	Cys	Pro	Glu	Arg	Leu	Ala	Ser	Cys	Arg	Ser	Ile	Asp	
130						135					140					
AAG	TTC	GCT	CAG	GGG	TGG	GGT	CCC	CTC	ACT	TAC	ACT	GAG	CCT	AAC	AGC	480
Lys	Phe	Ala	Gln	Gly	Trp	Gly	Pro	Leu	Thr	Tyr	Thr	Glu	Pro	Asn	Ser	
145					150					155					160	
TCG	GAC	CAG	AGG	CCC	TAC	TGC	TGG	CAC	TAC	GCG	CCT	CGA	CCG	TGT	GGT	528
Ser	Asp	Gln	Arg	Pro	Tyr	Cys	Trp	His	Tyr	Ala	Pro	Arg	Pro	Cys	Gly	
				165					170					175		
ATT	GTA	CCC	GCG	TCT	CAG	GTG	TGC	GGT	CCA	GTG	TAT	TGC	TTC	ACC	CCG	576
Ile	Val	Pro	Ala	Ser	Gln	Val	Cys	Gly	Pro	Val	Tyr	Cys	Phe	Thr	Pro	
			180					185					190			
AGC	CCT	GTT	GTG	GTG	GGG	ACG	ACC	GAT	CGG	TTT	GGT	GTC	CCC	ACG	TAT	624
Ser	Pro	Val	Val	Val	Gly	Thr	Thr	Asp	Arg	Phe	Gly	Val	Pro	Thr	Tyr	
		195					200					205				
AAC	TGG	GGG	GCG	AAC	GAC	TCG	GAT	GTG	CTG	ATT	CTC	AAC	AAC	ACG	CGG	672
Asn	Trp	Gly	Ala	Asn	Asp	Ser	Asp	Val	Leu	Ile	Leu	Asn	Asn	Thr	Arg	
	210					215					220					
CCG	CCG	CGA	GGC	AAC	TGG	TTC	GGC	TGT	ACA	TGG	ATG	AAT	GGC	ACT	GGG	720
Pro	Pro	Arg	Gly	Asn	Trp	Phe	Gly	Cys	Thr	Trp	Met	Asn	Gly	Thr	Gly	
225					230					235					240	
TTC	ACC	AAG	ACG	TGT	GGG	GGC	CCC	CCG	TGC	AAC	ATC	GGG	GGG	GCC	GGC	768
Phe	Thr	Lys	Thr	Cys	Gly	Gly	Pro	Pro	Cys	Asn	Ile	Gly	Gly	Ala	Gly	
				245					250					255		
AAC	AAC	ACC	TTG	ACC	TGC	CCC	ACT	GAC	TGT	TTT	CGG	AAG	CAC	CCC	GAG	816
Asn	Asn	Thr	Leu	Thr	Cys	Pro	Thr	Asp	Cys	Phe	Arg	Lys	His	Pro	Glu	
		260					265						270			
GCC	ACC	TAC	GCC	AGA	TGC	GGT	TCT	GGG	CCC	TGG	CTG	ACA	CCT	AGG	TGT	864
Ala	Thr	Tyr	Ala	Arg	Cys	Gly	Ser	Gly	Pro	Trp	Leu	Thr	Pro	Arg	Cys	
		275					280					285				
ATG	GTT	CAT	TAC	CCA	TAT	AGG	CTC	TGG	CAC	TAC	CCC	TGC	ACT	GTC	AAC	912
Met	Val	His	Tyr	Pro	Tyr	Arg	Leu	Trp	His	Tyr	Pro	Cys	Thr	Val	Asn	
	290					295					300					
TTC	ACC	ATC	TTC	AAG	GTT	AGG	ATG	TAC	GTG	GGG	GGC	GTG	GAG	CAC	AGG	960
Phe	Thr	Ile	Phe	Lys	Val	Arg	Met	Tyr	Val	Gly	Gly	Val	Glu	His	Arg	
305					310					315					320	
TTC	GAA	GCC	GCA	TGC	AAT	TGG	ACT	CGA	GGA	GAG	CGT	TGT	GAC	TTG	GAG	1008
Phe	Glu	Ala	Ala	Cys	Asn	Trp	Thr	Arg	Gly	Glu	Arg	Cys	Asp	Leu	Glu	
				325					330					335		
GAC	AGG	GAT	AGA	TCA	GAG	CTT	AGC	CCG	CTG	CTG	CTG	TCT	ACA	ACA	GAG	1056
Asp	Arg	Asp	Arg	Ser	Glu	Leu	Ser	Pro	Leu	Leu	Leu	Ser	Thr	Thr	Glu	
			340					345					350			
TGG	CAG	ATA	CTG	CCC	TGT	TCC	TTC	ACC	ACC	CTG	CCG	GCC	CTA	TCC	ACC	1104
Trp	Gln	Ile	Leu	Pro	Cys	Ser	Phe	Thr	Thr	Leu	Pro	Ala	Leu	Ser	Thr	
		355					360					365				
GGC	CTG	ATC	CAC	CTC	CAT	CAG	AAC	ATC	GTG	GAC	GTG	CAA	TAC	CTG	TAC	1152
Gly	Leu	Ile	His	Leu	His	Gln	Asn	Ile	Val	Asp	Val	Gln	Tyr	Leu	Tyr	
	370					375					380					



GGT GTA GGG TCG GCG GTT GTC TCC CTT GTC ATC AAA TGG GAG TAT GTC	1200
Gly Val Gly Ser Ala Val Val Ser Leu Val Ile Lys Trp Glu Tyr Val	
385 390 395 400	
CTG TTG CTC TTC CTT CTC CTG GCA GAC GCG CGC ATC TGC GCC TGC TTA	1248
Leu Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu	
405 410 415	
TGG ATG ATG CTG CTG ATA GCT CAA GCT GAG GCC GCC TTA GAG AAC CTG	1296
Trp Met Met Leu Leu Ile Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu	
420 425 430	
GTG GTC CTC AAT GCG GCG GCC GTG GCC GGG GCG CAT GGC ACT CTT TCC	1344
Val Val Leu Asn Ala Ala Ala Val Ala Gly Ala His Gly Thr Leu Ser	
435 440 445	
TTC CTT GTG TTC TTC TGT GCT GCC TGG TAC ATC AAG GGC AGG CTG GTC	1392
Phe Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val	
450 455 460	
CCT GGT GCG GCA TAC GCC TTC TAT GGC GTG TGG CCG CTG CTC CTG CTT	1440
Pro Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu	
465 470 475 480	
CTG CTG GCC TTA CCA CCA CGA GCT TAT GCC TAGTAA	1476
Leu Leu Ala Leu Pro Pro Arg Ala Tyr Ala	
485 490	

(2) INFORMATION FOR SEQ ID NO: 36:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 490 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val Val Ser	
1 5 10 15	
Gln Leu Leu Arg Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala	
20 25 30	
His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn	
35 40 45	
Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly	
50 55 60	
His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu	
65 70 75 80	
Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn	
85 90 95	
Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp	
100 105 110	

Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe  
 115 120 125  
 Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp  
 130 135 140  
 Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser  
 145 150 155 160  
 Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly  
 165 170 175  
 Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro  
 180 185 190  
 Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr  
 195 200 205  
 Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg  
 210 215 220  
 Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly  
 225 230 235 240  
 Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly  
 245 250 255  
 Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu  
 260 265 270  
 Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys  
 275 280 285  
 Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn  
 290 295 300  
 Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg  
 305 310 315 320  
 Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu  
 325 330 335  
 Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu  
 340 345 350  
 Trp Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr  
 355 360 365  
 Gly Leu Ile His Leu His Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr  
 370 375 380  
 Gly Val Gly Ser Ala Val Val Ser Leu Val Ile Lys Trp Glu Tyr Val  
 385 390 395 400  
 Leu Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu  
 405 410 415  
 Trp Met Met Leu Leu Ile Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu  
 420 425 430  
 Val Val Leu Asn Ala Ala Ala Val Ala Gly Ala His Gly Thr Leu Ser

435                      440                      445

Phe Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val  
450                      455                      460

Pro Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu  
465                      470                      475                      480

Leu Leu Ala Leu Pro Pro Arg Ala Tyr Ala  
485                      490

(2) INFORMATION FOR SEQ ID NO: 37:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1021 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 2..1018

- (ix) FEATURE:  
(A) NAME/KEY: mat\_peptide  
(B) LOCATION: 2..1015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

G ATC CCA CAA GCT GTC GTG GAC ATG GTG GCG GGG GCC CAT TGG GGA                      46  
Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly  
1                      5                      10                      15

GTC CTG GCG GGC CTC GCC TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG                      94  
Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys  
20                      25                      30

GTT TTG GTT GTG ATG CTA CTC TTT GCC GGC GTC GAC GGG CAT ACC CGC                      142  
Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg  
35                      40                      45

GTG TCA GGA GGG GCA GCA GCC TCC GAT ACC AGG GGC CTT GTG TCC CTC                      190  
Val Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu  
50                      55                      60

TTT AGC CCC GGG TCG GCT CAG AAA ATC CAG CTC GTA AAC ACC AAC GGC                      238  
Phe Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly  
65                      70                      75

AGT TGG CAC ATC AAC AGG ACT GCC CTG AAC TGC AAC GAC TCC CTC CAA                      286  
Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln  
80                      85                      90                      95

ACA GGG TTC TTT GCC GCA CTA TTC TAC AAA CAC AAA TTC AAC TCG TCT	334
Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser	
100 105 110	
GGA TGC CCA GAG CGC TTG GCC AGC TGT CGC TCC ATC GAC AAG TTC GCT	382
Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala	
115 120 125	
CAG GGG TGG GGT CCC CTC ACT TAC ACT GAG CCT AAC AGC TCG GAC CAG	430
Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln	
130 135 140	
AGG CCC TAC TGC TGG CAC TAC GCG CCT CGA CCG TGT GGT ATT GTA CCC	478
Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro	
145 150 155	
GCG TCT CAG GTG TGC GGT CCA GTG TAT TGC TTC ACC CCG AGC CCT GTT	526
Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val	
160 165 170 175	
GTG GTG GGG ACG ACC GAT CGG TTT GGT GTC CCC ACG TAT AAC TGG GGG	574
Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly	
180 185 190	
GCG AAC GAC TCG GAT GTG CTG ATT CTC AAC AAC ACG CGG CCG CCG CGA	622
Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg	
195 200 205	
GGC AAC TGG TTC GGC TGT ACA TGG ATG AAT GGC ACT GGG TTC ACC AAG	670
Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys	
210 215 220	
ACG TGT GGG GGC CCC CCG TGC AAC ATC GGG GGG GCC GGC AAC AAC ACC	718
Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr	
225 230 235	
TTG ACC TGC CCC ACT GAC TGT TTT CGG AAG CAC CCC GAG GCC ACC TAC	766
Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr	
240 245 250 255	
GCC AGA TGC GGT TCT GGG CCC TGG CTG ACA CCT AGG TGT ATG GTT CAT	814
Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His	
260 265 270	
TAC CCA TAT AGG CTC TGG CAC TAC CCC TGC ACT GTC AAC TTC ACC ATC	862
Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile	
275 280 285	
TTC AAG GTT AGG ATG TAC GTG GGG GGC GTG GAG CAC AGG TTC GAA GCC	910
Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala	
290 295 300	
GCA TGC AAT TGG ACT CGA GGA GAG CGT TGT GAC TTG GAG GAC AGG GAT	958
Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp	
305 310 315	
AGA TCA GAG CTT AGC CCG CTG CTG CTG TCT ACA ACA GAG TGG CAG AGT	1006
Arg Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu Trp Gln Ser	
320 325 330 335	
GGC AGA GCT TAATTA	1021

Gly Arg Ala

(2) INFORMATION FOR SEQ ID NO: 38:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 338 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val  
1 5 10 15  
Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val  
20 25 30  
Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg Val  
35 40 45  
Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu Phe  
50 55 60  
Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly Ser  
65 70 75 80  
Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr  
85 90 95  
Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser Gly  
100 105 110  
Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln  
115 120 125  
Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg  
130 135 140  
Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro Ala  
145 150 155 160  
Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val  
165 170 175  
Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly Ala  
180 185 190  
Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly  
195 200 205  
Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr  
210 215 220  
Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr Leu  
225 230 235 240  
Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr Ala  
245 250 255

Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His Tyr  
260 265 270

Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe  
275 280 285

Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala Ala  
290 295 300

Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp Arg  
305 310 315 320

Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu Trp Gln Ser Gly  
325 330 335

Arg Ala

00973025-101001

2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1034 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 2..1032

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide  
(B) LOCATION: 2..1029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

G ATC CCA CAA GCT GTC GTG GAC ATG GTG GCG GGG GCC CAT TGG GGA	46
Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly	
1 5 10 15	
GTC CTG GCG GGC CTC GCC TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG	94
Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys	
20 25 30	
GTT TTG GTT GTG ATG CTA CTC TTT GCC GGC GTC GAC GGG CAT ACC CGC	142
Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg	
35 40 45	
GTG TCA GGA GGG GCA GGA GCC TCC GAT ACC AGG GGC CTT GTG TCC CTC	190
Val Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu	
50 55 60	

TTT AGC CCC GGG TCG GCT CAG AAA ATC CAG CTC GTA AAC ACC AAC GGC	238
Phe Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly	
65 70 75	
AGT TGG CAC ATC AAC AGG ACT GCC CTG AAC TGC AAC GAC TCC CTC CAA	286
Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln	
80 85 90 95	
ACA GGG TTC TTT GCC GCA CTA TTC TAC AAA CAC AAA TTC AAC TCG TCT	334
Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser	
100 105 110	
GGA TGC CCA GAG CGC TTG GCC AGC TGT CGC TCC ATC GAC AAG TTC GCT	382
Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala	
115 120 125	
CAG GGG TGG GGT CCC CTC ACT TAC ACT GAG CCT AAC AGC TCG GAC CAG	430
Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln	
130 135 140	
AGG CCC TAC TGC TGG CAC TAC GCG CCT CGA CCG TGT GGT ATT GTA CCC	478
Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro	
145 150 155	
GGG TCT CAG GTG TGC GGT CCA GTG TAT TGC TTC ACC CCG AGC CCT GTT	526
Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val	
160 165 170 175	
GTG GTG GGG ACG ACC GAT CGG TTT GGT GTC CCC ACG TAT AAC TGG GGG	574
Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly	
180 185 190	
GGG AAC GAC TCG GAT GTG CTG ATT CTC AAC AAC ACG CGG CCG CCG CGA	622
Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg	
195 200 205	
GGC AAC TGG TTC GGC TGT ACA TGG ATG AAT GGC ACT GGG TTC ACC AAG	670
Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys	
210 215 220	
ACG TGT GGG GGC CCC CCG TGC AAC ATC GGG GGG GCC GGC AAC AAC ACC	718
Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr	
225 230 235	
TTG ACC TGC CCC ACT GAC TGT TTT CGG AAG CAC CCC GAG GCC ACC TAC	766
Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr	
240 245 250 255	
GCC AGA TGC GGT TCT GGG CCC TGG CTG ACA CCT AGG TGT ATG GTT CAT	814
Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His	
260 265 270	
TAC CCA TAT AGG CTC TGG CAC TAC CCC TGC ACT GTC AAC TTC ACC ATC	862
Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile	
275 280 285	
TTC AAG GTT AGG ATG TAC GTG GGG GGC GTG GAG CAC AGG TTC GAA GCC	910
Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala	
290 295 300	
GCA TGC AAT TGG ACT CGA GGA GAG CGT TGT GAC TTG GAG GAC AGG GAT	958
Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp	

305

310

315

AGA TCA GAG CTT AGC CCG CTG CTG CTG TCT ACA ACA GGT GAT CGA GGG  
 Arg Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Gly Asp Arg Gly  
 320 325 330 335

1006

CAG ACA CCA TCA CCA CCA TCA CTA AT AG  
 Gln Thr Pro Ser Pro Pro Ser Leu  
 340

1034

## (2) INFORMATION FOR SEQ ID NO: 40:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val  
 1 5 10 15  
 Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val  
 20 25 30  
 Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg Val  
 35 40 45  
 Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu Phe  
 50 55 60  
 Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly Ser  
 65 70 75 80  
 Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr  
 85 90 95  
 Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser Gly  
 100 105 110  
 Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln  
 115 120 125  
 Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg  
 130 135 140  
 Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro Ala  
 145 150 155 160  
 Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val  
 165 170 175  
 Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly Ala  
 180 185 190  
 Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly  
 195 200 205



Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr  
 210 215 220

Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr Leu  
 225 230 235 240

Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr Ala  
 245 250 255

Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His Tyr  
 260 265 270

Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe  
 275 280 285

Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala Ala  
 290 295 300

Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp Arg  
 305 310 315 320

Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Gly Asp Arg Gly Gln  
 325 330 335

Thr Pro Ser Pro Pro Ser Leu  
 340

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 945 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..942

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 1..939

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

ATG	GTG	GGG	AAC	TGG	GCT	AAG	GTT	TTG	GTT	GTG	ATG	CTA	CTC	TTT	GCC	48
Met	Val	Gly	Asn	Trp	Ala	Lys	Val	Leu	Val	Val	Met	Leu	Leu	Phe	Ala	
1				5				10						15		
GGC	GTC	GAC	GGG	CAT	ACC	CGC	GTG	TCA	GGA	GGG	GCA	GCA	GCC	TCC	GAT	96
Gly	Val	Asp	Gly	His	Thr	Arg	Val	Ser	Gly	Gly	Ala	Ala	Ala	Ser	Asp	
			20					25						30		

ACC AGG GGC CTT GTG TCC CTC TTT AGC CCC GGG TCG GCT CAG AAA ATC	144
Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile	
35 40 45	
CAG CTC GTA AAC ACC AAC GGC AGT TGG CAC ATC AAC AGG ACT GCC CTG	192
Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu	
50 55 60	
AAC TGC AAC GAC TCC CTC CAA ACA GGG TTC TTT GCC GCA CTA TTC TAC	240
Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr	
65 70 75 80	
AAA CAC AAA TTC AAC TCG TCT GGA TGC CCA GAG CGC TTG GCC AGC TGT	288
Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys	
85 90 95	
CGC TCC ATC GAC AAG TTC GCT CAG GGG TGG GGT CCC CTC ACT TAC ACT	336
Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr	
100 105 110	
GAG CCT AAC AGC TCG GAC CAG AGG CCC TAC TGC TGG CAC TAC GCG CCT	384
Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro	
115 120 125	
CGA CCG TGT GGT ATT GTA CCC GCG TCT CAG GTG TGC GGT CCA GTG TAT	432
Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr	
130 135 140	
TGC TTC ACC CCG AGC CCT GTT GTG GTG GGG ACG ACC GAT CGG TTT GGT	480
Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly	
145 150 155 160	
GTC CCC ACG TAT AAC TGG GGG GCG AAC GAC TCG GAT GTG CTG ATT CTC	528
Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu	
165 170 175	
AAC AAC ACG CGG CCG CCG CGA GGC AAC TGG TTC GGC TGT ACA TGG ATG	576
Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met	
180 185 190	
AAT GGC ACT GGG TTC ACC AAG ACG TGT GGG GGC CCC CCG TGC AAC ATC	624
Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile	
195 200 205	
GGG GGG GCC GGC AAC AAC ACC TTG ACC TGC CCC ACT GAC TGT TTT CGG	672
Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg	
210 215 220	
AAG CAC CCC GAG GCC ACC TAC GCC AGA TGC GGT TCT GGG CCC TGG CTG	720
Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu	
225 230 235 240	
ACA CCT AGG TGT ATG GTT CAT TAC CCA TAT AGG CTC TGG CAC TAC CCC	768
Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro	
245 250 255	
TGC ACT GTC AAC TTC ACC ATC TTC AAG GTT AGG ATG TAC GTG GGG GGC	816
Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly	
260 265 270	
GTG GAG CAC AGG TTC GAA GCC GCA TGC AAT TGG ACT CGA GGA GAG CGT	864

Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg  
275 280 285

TGT GAC TTG GAG GAC AGG GAT AGA TCA GAG CTT AGC CCG CTG CTG CTG 912  
Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu  
290 295 300

TCT ACA ACA GAG TGG CAG AGC TTA ATT AAT TAG 945  
Ser Thr Thr Glu Trp Gln Ser Leu Ile Asn  
305 310

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 314 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala  
1 5 10 15  
Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp  
20 25 30  
Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile  
35 40 45  
Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu  
50 55 60  
Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr  
65 70 75 80  
Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys  
85 90 95  
Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr  
100 105 110  
Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro  
115 120 125  
Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr  
130 135 140  
Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly  
145 150 155 160  
Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu  
165 170 175  
Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met  
180 185 190  
Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile  
195 200 205

09073005100001

Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg  
 210 215 220  
 Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu  
 225 230 235 240  
 Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro  
 245 250 255  
 Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly  
 260 265 270  
 Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg  
 275 280 285  
 Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu  
 290 295 300  
 Ser Thr Thr Glu Trp Gln Ser Leu Ile Asn  
 305 310

2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 961 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..958

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..955

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

ATG GTG GGG AAC TGG GCT AAG GTT TTG GTT GTG ATG CTA CTC TTT GCC	48
Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala	
1 5 10 15	
GGC GTC GAC GGG CAT ACC CGC GTG TCA GGA GGG GCA GCA GCC TCC GAT	96
Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp	
20 25 30	
ACC AGG GGC CTT GTG TCC CTC TTT AGC CCC GGG TCG GCT CAG AAA ATC	144
Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile	
35 40 45	
CAG CTC GTA AAC ACC AAC GGC AGT TGG CAC ATC AAC AGG ACT GCC CTG	192

Gln	Leu	Val	Asn	Thr	Asn	Gly	Ser	Trp	His	Ile	Asn	Arg	Thr	Ala	Leu		
	50					55					60						
AAC	TGC	AAC	GAC	TCC	CTC	CAA	ACA	GGG	TTC	TTT	GCC	GCA	CTA	TTC	TAC	240	
Asn	Cys	Asn	Asp	Ser	Leu	Gln	Thr	Gly	Phe	Phe	Ala	Ala	Leu	Phe	Tyr	80	
65					70				75								
AAA	CAC	AAA	TTC	AAC	TCG	TCT	GGA	TGC	CCA	GAG	CGC	TTG	GCC	AGC	TGT	288	
Lys	His	Lys	Phe	Asn	Ser	Ser	Gly	Cys	Pro	Glu	Arg	Leu	Ala	Ser	Cys	95	
				85					90								
CGC	TCC	ATC	GAC	AAG	TTC	GCT	CAG	GGG	TGG	GGT	CCC	CTC	ACT	TAC	ACT	336	
Arg	Ser	Ile	Asp	Lys	Phe	Ala	Gln	Gly	Trp	Gly	Pro	Leu	Thr	Tyr	Thr	110	
			100					105									
GAG	CCT	AAC	AGC	TCG	GAC	CAG	AGG	CCC	TAC	TGC	TGG	CAC	TAC	GCG	CCT	384	
Glu	Pro	Asn	Ser	Ser	Asp	Gln	Arg	Pro	Tyr	Cys	Trp	His	Tyr	Ala	Pro	125	
		115					120										
CGA	CCG	TGT	GGT	ATT	GTA	CCC	GCG	TCT	CAG	GTG	TGC	GGT	CCA	GTG	TAT	432	
Arg	Pro	Cys	Gly	Ile	Val	Pro	Ala	Ser	Gln	Val	Cys	Gly	Pro	Val	Tyr	140	
	130					135											
TGC	TTC	ACC	CCG	AGC	CCT	GTT	GTG	GTG	GGG	ACG	ACC	GAT	CGG	TTT	GGT	480	
Cys	Phe	Thr	Pro	Ser	Pro	Val	Val	Val	Gly	Thr	Thr	Asp	Arg	Phe	Gly	160	
145					150				155								
GTC	CCC	ACG	TAT	AAC	TGG	GGG	GCG	AAC	GAC	TCG	GAT	GTG	CTG	ATT	CTC	528	
Val	Pro	Thr	Tyr	Asn	Trp	Gly	Ala	Asn	Asp	Ser	Asp	Val	Leu	Ile	Leu	175	
				165					170								
AAC	AAC	ACG	CGG	CCG	CCG	CGA	GGC	AAC	TGG	TTC	GGC	TGT	ACA	TGG	ATG	576	
Asn	Asn	Thr	Arg	Pro	Pro	Arg	Gly	Asn	Trp	Phe	Gly	Cys	Thr	Trp	Met	190	
			180					185									
AAT	GGC	ACT	GGG	TTC	ACC	AAG	ACG	TGT	GGG	GGC	CCC	CCG	TGC	AAC	ATC	624	
Asn	Gly	Thr	Gly	Phe	Thr	Lys	Thr	Cys	Gly	Gly	Pro	Pro	Cys	Asn	Ile	205	
		195					200										
GGG	GGG	GCC	GGC	AAC	AAC	ACC	TTG	ACC	TGC	CCC	ACT	GAC	TGT	TTT	CGG	672	
Gly	Gly	Ala	Gly	Asn	Asn	Thr	Leu	Thr	Cys	Pro	Thr	Asp	Cys	Phe	Arg	220	
	210					215											
AAG	CAC	CCC	GAG	GCC	ACC	TAC	GCC	AGA	TGC	GGT	TCT	GGG	CCC	TGG	CTG	720	
Lys	His	Pro	Glu	Ala	Thr	Tyr	Ala	Arg	Cys	Gly	Ser	Gly	Pro	Trp	Leu	240	
225					230				235								
ACA	CCT	AGG	TGT	ATG	GTT	CAT	TAC	CCA	TAT	AGG	CTC	TGG	CAC	TAC	CCC	768	
Thr	Pro	Arg	Cys	Met	Val	His	Tyr	Pro	Tyr	Arg	Leu	Trp	His	Tyr	Pro	255	
				245					250								
TGC	ACT	GTC	AAC	TTC	ACC	ATC	TTC	AAG	GTT	AGG	ATG	TAC	GTG	GGG	GGC	816	
Cys	Thr	Val	Asn	Phe	Thr	Ile	Phe	Lys	Val	Arg	Met	Tyr	Val	Gly	Gly	270	
			260					265									
GTG	GAG	CAC	AGG	TTC	GAA	GCC	GCA	TGC	AAT	TGG	ACT	CGA	GGA	GAG	CGT	864	
Val	Glu	His	Arg	Phe	Glu	Ala	Ala	Cys	Asn	Trp	Thr	Arg	Gly	Glu	Arg	285	
		275					280										
TGT	GAC	TTG	GAG	GAC	AGG	GAT	AGA	TCA	GAG	CTT	AGC	CCG	CTG	CTG	CTG	912	
Cys	Asp	Leu	Glu	Asp	Arg	Asp	Arg	Ser	Glu	Leu	Ser	Pro	Leu	Leu	Leu		

290	295	300	
TCT ACA ACA GGT GAT CGA GGG CAG ACA CCA TCA CCA CCA TCA CTA A			958
Ser Thr Thr Gly Asp Arg Gly Gln Thr Pro Ser Pro Pro Ser Leu			
305	310	315	961
TAG			

(2) INFORMATION FOR SEQ ID NO: 44:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 319 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala  
 1 5 10 15  
 Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp  
 20 25 30  
 Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile  
 35 40 45  
 Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu  
 50 55 60  
 Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr  
 65 70 75 80  
 Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys  
 85 90 95  
 Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr  
 100 105 110  
 Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro  
 115 120 125  
 Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr  
 130 135 140  
 Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly  
 145 150 155 160  
 Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu  
 165 170 175  
 Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met  
 180 185 190  
 Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile  
 195 200 205  
 Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg  
 210 215 220  
 Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu

225	230	235	240
Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro	245	250	255
Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly	260	265	270
Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg	275	280	285
Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu	290	295	300
Ser Thr Thr Gly Asp Arg Gly Gln Thr Pro Ser Pro Pro Ser Leu	305	310	315

02) INFORMATION FOR SEQ ID NO: 45:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1395 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..1392

- (ix) FEATURE:  
 (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 1..1389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

ATG GTG GCG GGG GCC CAT TGG GGA GTC CTG GCG GGC CTC GCC TAC TAT	48
Met Val Ala Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr	
1 5 10 15	
TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG GTT GTG ATG CTA CTC TTT	96
Ser Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe	
20 25 30	
GCC GGC GTC GAC GGG CAT ACC CGC GTG TCA GGA GGG GCA GCA GCC TCC	144
Ala Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser	
35 40 45	
GAT ACC AGG GGC CTT GTG TCC CTC TTT AGC CCC GGG TCG GCT CAG AAA	192
Asp Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys	
50 55 60	
ATC CAG CTC GTA AAC ACC AAC GGC AGT TGG CAC ATC AAC AGG ACT GCC	240
Ile Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala	
65 70 75 80	

CTG AAC TGC AAC GAC TCC CTC CAA ACA GGG TTC TTT GCC GCA CTA TTC	288
Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe	
85 90 95	
TAC AAA CAC AAA TTC AAC TCG TCT GGA TGC CCA GAG CGC TTG GCC AGC	336
Tyr Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser	
100 105 110	
TGT CGC TCC ATC GAC AAG TTC GCT CAG GGG TGG GGT CCC CTC ACT TAC	384
Cys Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr	
115 120 125	
ACT GAG CCT AAC AGC TCG GAC CAG AGG CCC TAC TGC TGG CAC TAC GCG	432
Thr Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala	
130 135 140	
GCT CGA CCG TGT GGT ATT GTA CCC GCG TCT CAG GTG TGC GGT CCA GTG	480
Pro Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val	
145 150 155 160	
TAT TGC TTC ACC CCG AGC CCT GTT GTG GTG GGG ACG ACC GAT CGG TTT	528
Tyr Cys Phe Thr Pro Ser Pro Val Val Gly Thr Thr Asp Arg Phe	
165 170 175	
GGT GTC CCC ACG TAT AAC TGG GGG GCG AAC GAC TCG GAT GTG CTG ATT	576
Gly Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile	
180 185 190	
CTC AAC AAC ACG CGG CCG CCG CGA GGC AAC TGG TTC GGC TGT ACA TGG	624
Leu Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp	
195 200 205	
ATG AAT GGC ACT GGG TTC ACC AAG ACG TGT GGG GGC CCC CCG TGC AAC	672
Met Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn	
210 215 220	
ATC GGG GGG GCC GGC AAC AAC ACC TTG ACC TGC CCC ACT GAC TGT TTT	720
Ile Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe	
225 230 235 240	
CGG AAG CAC CCC GAG GCC ACC TAC GCC AGA TGC GGT TCT GGG CCC TGG	768
Arg Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp	
245 250 255	
CTG ACA CCT AGG TGT ATG GTT CAT TAC CCA TAT AGG CTC TGG CAC TAC	816
Leu Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr	
260 265 270	
CCC TGC ACT GTC AAC TTC ACC ATC TTC AAG GTT AGG ATG TAC GTG GGG	864
Pro Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly	
275 280 285	
GGC GTG GAG CAC AGG TTC GAA GCC GCA TGC AAT TGG ACT CGA GGA GAG	912
Gly Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu	
290 295 300	
CGT TGT GAC TTG GAG GAC AGG GAT AGA TCA GAG CTT AGC CCG CTG CTG	960
Arg Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu	
305 310 315 320	
CTG TCT ACA ACA GAG TGG CAG ATA CTG CCC TGT TCC TTC ACC ACC CTG	1008



Leu	Ser	Thr	Thr	Glu	Trp	Gln	Ile	Leu	Pro	Cys	Ser	Phe	Thr	Thr	Leu		
				325					330						335		
CCG	GCC	CTA	TCC	ACC	GGC	CTG	ATC	CAC	CTC	CAT	CAG	AAC	ATC	GTG	GAC		1056
Pro	Ala	Leu	Ser	Thr	Gly	Leu	Ile	His	Leu	His	Gln	Asn	Ile	Val	Asp		
				340				345					350				
GTG	CAA	TAC	CTG	TAC	GGT	GTA	GGG	TCG	GCG	GTT	GTC	TCC	CTT	GTC	ATC		1104
Val	Gln	Tyr	Leu	Tyr	Gly	Val	Gly	Ser	Ala	Val	Val	Ser	Leu	Val	Ile		
			355				360					365					
AAA	TGG	GAG	TAT	GTC	CTG	TTG	CTC	TTC	CTT	CTC	CTG	GCA	GAC	GCG	CGC		1152
Lys	Trp	Glu	Tyr	Val	Leu	Leu	Leu	Phe	Leu	Leu	Leu	Ala	Asp	Ala	Arg		
						375					380						
ATC	TGC	GCC	TGC	TTA	TGG	ATG	ATG	CTG	CTG	ATA	GCT	CAA	GCT	GAG	GCC		1200
Ile	Cys	Ala	Cys	Leu	Trp	Met	Met	Leu	Leu	Ile	Ala	Gln	Ala	Glu	Ala		
						390				395					400		
GCC	TTA	GAG	AAC	CTG	GTG	GTC	CTC	AAT	GCG	GCG	GCC	GTG	GCC	GGG	GCG		1248
Ala	Leu	Glu	Asn	Leu	Val	Val	Leu	Asn	Ala	Ala	Ala	Val	Ala	Gly	Ala		
				405				410						415			
GAT	GGC	ACT	CTT	TCC	TTC	CTT	GTG	TTC	TTC	TGT	GCT	GCC	TGG	TAC	ATC		1296
His	Gly	Thr	Leu	Ser	Phe	Leu	Val	Phe	Phe	Cys	Ala	Ala	Trp	Tyr	Ile		
				420				425					430				
AAG	GGC	AGG	CTG	GTC	CCT	GGT	GCG	GCA	TAC	GCC	TTC	TAT	GGC	GTG	TGG		1344
Lys	Gly	Arg	Leu	Val	Pro	Gly	Ala	Ala	Tyr	Ala	Phe	Tyr	Gly	Val	Trp		
				435			440					445					
CCG	CTG	CTC	CTG	CTT	CTG	CTG	GCC	TTA	CCA	CCA	CGA	GCT	TAT	GCC	TAGTAA		1395
Pro	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Leu	Pro	Pro	Arg	Ala	Tyr	Ala			
				450			455				460						

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 463 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Met	Val	Ala	Gly	Ala	His	Trp	Gly	Val	Leu	Ala	Gly	Leu	Ala	Tyr	Tyr
1				5				10						15	
Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val	Leu	Val	Val	Met	Leu	Leu	Phe
			20				25					30			
Ala	Gly	Val	Asp	Gly	His	Thr	Arg	Val	Ser	Gly	Gly	Ala	Ala	Ala	Ser
			35				40					45			
Asp	Thr	Arg	Gly	Leu	Val	Ser	Leu	Phe	Ser	Pro	Gly	Ser	Ala	Gln	Lys
			50			55				60					
Ile	Gln	Leu	Val	Asn	Thr	Asn	Gly	Ser	Trp	His	Ile	Asn	Arg	Thr	Ala
65				70				75						80	

Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe  
 85 90 95  
 Tyr Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser  
 100 105 110  
 Cys Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr  
 115 120 125  
 Thr Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala  
 130 135 140  
 Pro Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val  
 145 150 155 160  
 Tyr Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe  
 165 170 175  
 Gly Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile  
 180 185 190  
 Leu Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp  
 195 200 205  
 Met Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn  
 210 215 220  
 Ile Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe  
 225 230 235 240  
 Arg Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp  
 245 250 255  
 Leu Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr  
 260 265 270  
 Pro Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly  
 275 280 285  
 Gly Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu  
 290 295 300  
 Arg Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu  
 305 310 315 320  
 Leu Ser Thr Thr Glu Trp Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu  
 325 330 335  
 Pro Ala Leu Ser Thr Gly Leu Ile His Leu His Gln Asn Ile Val Asp  
 340 345 350  
 Val Gln Tyr Leu Tyr Gly Val Gly Ser Ala Val Val Ser Leu Val Ile  
 355 360 365  
 Lys Trp Glu Tyr Val Leu Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg  
 370 375 380  
 Ile Cys Ala Cys Leu Trp Met Met Leu Leu Ile Ala Gln Ala Glu Ala  
 385 390 395 400  
 Ala Leu Glu Asn Leu Val Val Leu Asn Ala Ala Val Ala Gly Ala

405                      410                      415  
 His Gly Thr Leu Ser Phe Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile  
                     420                      425                      430  
 Lys Gly Arg Leu Val Pro Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp  
                     435                      440                      445  
 Pro Leu Leu Leu Leu Leu Leu Ala Leu Pro Pro Arg Ala Tyr Ala  
                     450                      455                      460

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2082 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2079

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..2076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

AAT TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC	48
Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1                      5                      10                      15	
GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG	96
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20                      25                      30	
GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA	144
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35                      40                      45	
ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG	192
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
50                      55                      60	
CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG	240
Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	
65                      70                      75                      80	
TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG	288
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	
85                      90                      95	

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TAT	GAG	GCA	GCG	GAC	ATG	ATC	ATG	CAC	ACC	CCC	GGG	TGC	GTG	CCC	TGC	336
Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	
		100						105					110			
GTT	CGG	GAG	AAC	AAC	TCT	TCC	CGC	TGC	TGG	GTA	GCG	CTC	ACC	CCC	ACG	384
Val	Arg	Glu	Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	
	115						120					125				
CTC	GCA	GCT	AGG	AAC	GCC	AGC	GTC	CCC	ACC	ACG	ACA	ATA	CGA	CGC	CAC	432
Leu	Ala	Ala	Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	
	130					135					140					
GTC	GAT	TTG	CTC	GTT	GGG	GCG	GCT	GCT	TTC	TGT	TCC	GCT	ATG	TAC	GTG	480
Val	Asp	Leu	Leu	Val	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	
145				150					155						160	
GGG	GAC	CTC	TGC	GGA	TCT	GTC	TTC	CTC	GTC	TCC	CAG	CTG	TTC	ACC	ATC	528
Gly	Asp	Leu	Cys	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Ile	
			165					170						175		
TCG	CCT	CGC	CGG	CAT	GAG	ACG	GTG	CAG	GAC	TGC	AAT	TGC	TCA	ATC	TAT	576
Ser	Pro	Arg	Arg	His	Glu	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	
		180						185					190			
CCC	GGC	CAC	ATA	ACG	GGT	CAC	CGT	ATG	GCT	TGG	GAT	ATG	ATG	ATG	AAC	624
Pro	Gly	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	
		195					200					205				
TGG	TCG	CCT	ACA	ACG	GCC	CTG	GTG	GTA	TCG	CAG	CTG	CTC	CGG	ATC	CCA	672
Trp	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro	
	210					215					220					
CAA	GCT	GTC	GTG	GAC	ATG	GTG	GCG	GGG	GCC	CAT	TGG	GGA	GTC	CTG	GCG	720
Gln	Ala	Val	Val	Asp	Met	Val	Ala	Gly	Ala	His	Trp	Gly	Val	Leu	Ala	
225				230						235				240		
GGC	CTC	GCC	TAC	TAT	TCC	ATG	GTG	GGG	AAC	TGG	GCT	AAG	GTT	TTG	GTT	768
Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val	Leu	Val	
			245					250						255		
GTG	ATG	CTA	CTC	TTT	GCC	GGC	GTC	GAC	GGG	CAT	ACC	CGC	GTG	TCA	GGA	816
Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly	His	Thr	Arg	Val	Ser	Gly	
		260					265						270			
GGG	GCA	GCA	GCC	TCC	GAT	ACC	AGG	GGC	CTT	GTG	TCC	CTC	TTT	AGC	CCC	864
Gly	Ala	Ala	Ala	Ser	Asp	Thr	Arg	Gly	Leu	Val	Ser	Leu	Phe	Ser	Pro	
		275					280					285				
GGG	TCG	GCT	CAG	AAA	ATC	CAG	CTC	GTA	AAC	ACC	AAC	GGC	AGT	TGG	CAC	912
Gly	Ser	Ala	Gln	Lys	Ile	Gln	Leu	Val	Asn	Thr	Asn	Gly	Ser	Trp	His	
	290					295					300					
ATC	AAC	AGG	ACT	GCC	CTG	AAC	TGC	AAC	GAC	TCC	CTC	CAA	ACA	GGG	TTC	960
Ile	Asn	Arg	Thr	Ala	Leu	Asn	Cys	Asn	Asp	Ser	Leu	Gln	Thr	Gly	Phe	
305				310					315					320		
TTT	GCC	GCA	CTA	TTC	TAC	AAA	CAC	AAA	TTC	AAC	TCG	TCT	GGA	TGC	CCA	1008
Phe	Ala	Ala	Leu	Phe	Tyr	Lys	His	Lys	Phe	Asn	Ser	Ser	Gly	Cys	Pro	
			325					330						335		
GAG	CGC	TTG	GCC	AGC	TGT	CGC	TCC	ATC	GAC	AAG	TTC	GCT	CAG	GGG	TGG	1056

Glu	Arg	Leu	Ala	Ser	Cys	Arg	Ser	Ile	Asp	Lys	Phe	Ala	Gln	Gly	Trp	
			340					345					350			
GGT	CCC	CTC	ACT	TAC	ACT	GAG	CCT	AAC	AGC	TCG	GAC	CAG	AGG	CCC	TAC	1104
Gly	Pro	Leu	Thr	Tyr	Thr	Glu	Pro	Asn	Ser	Ser	Asp	Gln	Arg	Pro	Tyr	
		355					360					365				
TGC	TGG	CAC	TAC	GCG	CCT	CGA	CCG	TGT	GGT	ATT	GTA	CCC	GCG	TCT	CAG	1152
Cys	Trp	His	Tyr	Ala	Pro	Arg	Pro	Cys	Gly	Ile	Val	Pro	Ala	Ser	Gln	
	370					375					380					
GTG	TGC	GGT	CCA	GTG	TAT	TGC	TTC	ACC	CCG	AGC	CCT	GTT	GTG	GTG	GGG	1200
Val	Cys	Gly	Pro	Val	Tyr	Cys	Phe	Thr	Pro	Ser	Pro	Val	Val	Val	Gly	
385					390					395					400	
ACG	ACC	GAT	CGG	TTT	GGT	GTC	CCC	ACG	TAT	AAC	TGG	GGG	GCG	AAC	GAC	1248
Thr	Thr	Asp	Arg	Phe	Gly	Val	Pro	Thr	Tyr	Asn	Trp	Gly	Ala	Asn	Asp	
				405					410					415		
TCG	GAT	GTG	CTG	ATT	CTC	AAC	AAC	ACG	CGG	CCG	CCG	CGA	GGC	AAC	TGG	1296
Ser	Asp	Val	Leu	Ile	Leu	Asn	Asn	Thr	Arg	Pro	Pro	Arg	Gly	Asn	Trp	
			420					425					430			
ATC	GGC	TGT	ACA	TGG	ATG	AAT	GGC	ACT	GGG	TTC	ACC	AAG	ACG	TGT	GGG	1344
Phe	Gly	Cys	Thr	Trp	Met	Asn	Gly	Thr	Gly	Phe	Thr	Lys	Thr	Cys	Gly	
		435					440					445				
GGC	CCC	CCG	TGC	AAC	ATC	GGG	GGG	GCC	GGC	AAC	AAC	ACC	TTG	ACC	TGC	1392
Gly	Pro	Pro	Cys	Asn	Ile	Gly	Gly	Ala	Gly	Asn	Asn	Thr	Leu	Thr	Cys	
	450					455					460					
CCC	ACT	GAC	TGT	TTT	CGG	AAG	CAC	CCC	GAG	GCC	ACC	TAC	GCC	AGA	TGC	1440
Pro	Thr	Asp	Cys	Phe	Arg	Lys	His	Pro	Glu	Ala	Thr	Tyr	Ala	Arg	Cys	
465					470					475					480	
GGT	TCT	GGG	CCC	TGG	CTG	ACA	CCT	AGG	TGT	ATG	GTT	CAT	TAC	CCA	TAT	1488
Gly	Ser	Gly	Pro	Trp	Leu	Thr	Pro	Arg	Cys	Met	Val	His	Tyr	Pro	Tyr	
			485					490						495		
AGG	CTC	TGG	CAC	TAC	CCC	TGC	ACT	GTC	AAC	TTC	ACC	ATC	TTC	AAG	GTT	1536
Arg	Leu	Trp	His	Tyr	Pro	Cys	Thr	Val	Asn	Phe	Thr	Ile	Phe	Lys	Val	
			500					505					510			
AGG	ATG	TAC	GTG	GGG	GGC	GTG	GAG	CAC	AGG	TTC	GAA	GCC	GCA	TGC	AAT	1584
Arg	Met	Tyr	Val	Gly	Gly	Val	Glu	His	Arg	Phe	Glu	Ala	Ala	Cys	Asn	
		515					520					525				
TGG	ACT	CGA	GGA	GAG	CGT	TGT	GAC	TTG	GAG	GAC	AGG	GAT	AGA	TCA	GAG	1632
Trp	Thr	Arg	Gly	Glu	Arg	Cys	Asp	Leu	Glu	Asp	Arg	Asp	Arg	Ser	Glu	
		530				535					540					
CTT	AGC	CCG	CTG	CTG	CTG	TCT	ACA	ACA	GAG	TGG	CAG	ATA	CTG	CCC	TGT	1680
Leu	Ser	Pro	Leu	Leu	Leu	Ser	Thr	Thr	Glu	Trp	Gln	Ile	Leu	Pro	Cys	
545					550					555					560	
TCC	TTC	ACC	ACC	CTG	CCG	GCC	CTA	TCC	ACC	GGC	CTG	ATC	CAC	CTC	CAT	1728
Ser	Phe	Thr	Thr	Leu	Pro	Ala	Leu	Ser	Thr	Gly	Leu	Ile	His	Leu	His	
				565				570						575		
CAG	AAC	ATC	GTG	GAC	GTG	CAA	TAC	CTG	TAC	GGT	GTA	GGG	TCG	GCG	GTT	1776
Gln	Asn	Ile	Val	Asp	Val	Gln	Tyr	Leu	Tyr	Gly	Val	Gly	Ser	Ala	Val	
			580					585					590			

GTC TCC CTT GTC ATC AAA TGG GAG TAT GTC CTG TTG CTC TTC CTT CTC	1824
Val Ser Leu Val Ile Lys Trp Glu Tyr Val Leu Leu Leu Phe Leu Leu	
595 600 605	
CTG GCA GAC GCG CGC ATC TGC GCC TGC TTA TGG ATG ATG CTG CTG ATA	1872
Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu Trp Met Met Leu Leu Ile	
610 615 620	
GCT CAA GCT GAG GCC GCC TTA GAG AAC CTG GTG GTC CTC AAT GCG GCG	1920
Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu Val Val Leu Asn Ala Ala	
625 630 635 640	
GCC GTG GCC GGG GCG CAT GGC ACT CTT TCC TTC CTT GTG TTC TTC TGT	1968
Ala Val Ala Gly Ala His Gly Thr Leu Ser Phe Leu Val Phe Phe Cys	
645 650 655	
GCT GCC TGG TAC ATC AAG GGC AGG CTG GTC CCT GGT GCG GCA TAC GCC	2016
Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val Pro Gly Ala Ala Tyr Ala	
660 665 670	
TTC TAT GGC GTG TGG CCG CTG CTC CTG CTT CTG CTG GCC TTA CCA CCA	2064
Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu Leu Ala Leu Pro Pro	
675 680 685	
GGA GCT TAT GCC TAGTAA	2082
Arg Ala Tyr Ala	
690	

(2) INFORMATION FOR SEQ ID NO: 48:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 692 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
'1 5 10 15	
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20 25 30	
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35 40 45	
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
50 55 60	
Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	
65 70 75 80	
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	
85 90 95	
Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys	
100 105 110	

Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr  
115 120 125

Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His  
130 135 140

Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val  
145 150 155 160

Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile  
165 170 175

Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr  
180 185 190

Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn  
195 200 205

Trp Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro  
210 215 220

Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala  
225 230 235 240

Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Val  
245 250 255

Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg Val Ser Gly  
260 265 270

Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu Phe Ser Pro  
275 280 285

Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly Ser Trp His  
290 295 300

Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe  
305 310 315 320

Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser Gly Cys Pro  
325 330 335

Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp  
340 345 350

Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr  
355 360 365

Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro Ala Ser Gln  
370 375 380

Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val Val Gly  
385 390 395 400

Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp  
405 410 415

Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp  
420 425 430

Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly





(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..2430

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: 1..2427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT AAC ACC AAC	48
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn	
1 5 10 15	
CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT GGT	96
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly	
20 25 30	
GGA GTT TAC CTG TTG CCG CGC AGG GGC CCC AGG TTG GGT GTG CGC GCG	144
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala	
35 40 45	
ACT AGG AAG ACT TCC GAG CGG TCG CAA CCT CGT GGG AGG CGA CAA CCT	192
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro	
50 55 60	
ATC CCC AAG GCT CGC CGA CCC GAG GGT AGG GCC TGG GCT CAG CCC GGG	240
Phe Pro Lys Ala Arg Arg Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly	
65 70 75 80	
TAC CCT TGG CCC CTC TAT GGC AAT GAG GGC ATG GGG TGG GCA GGA TGG	288
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp	
85 90 95	
CTC CTG TCA CCC CGC GGC TCT CGG CCT AGT TGG GGC CCT ACA GAC CCC	336
Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro	
100 105 110	
CGG CGT AGG TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC	384
Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys	
115 120 125	
GGC TTC GCC GAC CTC GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA	432
Gly Phe Ala Asp Leu Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu	
130 135 140	
GGG GGC GCT GCC AGG GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC	480
Gly Gly Ala Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp	
145 150 155 160	
GGC GTG AAC TAT GCA ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC	528
Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile	
165 170 175	
TTC CTC TTG GCT TTG CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT	576
Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr	

180								185								190								
GAA	GTG	CGC	AAC	GTG	TCC	GGG	ATG	TAC	CAT	GTC	ACG	AAC	GAC	TGC	TCC		624							
Glu	Val	Arg	Asn	Val	Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser									
		195					200					205												
AAC	TCA	AGC	ATT	GTG	TAT	GAG	GCA	GCG	GAC	ATG	ATC	ATG	CAC	ACC	CCC	672								
Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro									
	210					215					220													
GGG	TGC	GTG	CCC	TGC	GTT	CGG	GAG	AAC	AAC	TCT	TCC	CGC	TGC	TGG	GTA	720								
Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val									
225					230					235					240									
GCG	CTC	ACC	CCC	ACG	CTC	GCA	GCT	AGG	AAC	GCC	AGC	GTC	CCC	ACC	ACG	768								
Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr									
				245					250					255										
AGA	ATA	CGA	CGC	CAC	GTC	GAT	TTG	CTC	GTT	GGG	GCG	GCT	GCT	TTC	TGT	816								
Thr	Ile	Arg	Arg	His	Val	Asp	Leu	Leu	Val	Gly	Ala	Ala	Ala	Phe	Cys									
			260				265						270											
TGC	GCT	ATG	TAC	GTG	GGG	GAC	CTC	TGC	GGA	TCT	GTC	TTC	CTC	GTC	TCC	864								
Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu	Cys	Gly	Ser	Val	Phe	Leu	Val	Ser									
		275					280					285												
CAG	CTG	TTC	ACC	ATC	TCG	CCT	CGC	CGG	CAT	GAG	ACG	GTG	CAG	GAC	TGC	912								
Gln	Leu	Phe	Thr	Ile	Ser	Pro	Arg	Arg	His	Glu	Thr	Val	Gln	Asp	Cys									
		290				295					300													
AAT	TGC	TCA	ATC	TAT	CCC	GGC	CAC	ATA	ACG	GGT	CAC	CGT	ATG	GCT	TGG	960								
Asn	Cys	Ser	Ile	Tyr	Pro	Gly	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp									
					310					315					320									
GAT	ATG	ATG	ATG	AAC	TGG	TCG	CCT	ACA	ACG	GCC	CTG	GTG	GTA	TCG	CAG	1008								
Asp	Met	Met	Met	Asn	Trp	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ser	Gln									
				325					330					335										
CTG	CTC	CGG	ATC	CCA	CAA	GCT	GTC	GTG	GAC	ATG	GTG	GCG	GGG	GCC	CAT	1056								
Leu	Leu	Arg	Ile	Pro	Gln	Ala	Val	Val	Asp	Met	Val	Ala	Gly	Ala	His									
			340				345						350											
TGG	GGA	GTC	CTG	GCG	GGC	CTC	GCC	TAC	TAT	TCC	ATG	GTG	GGG	AAC	TGG	1104								
Trp	Gly	Val	Leu	Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp									
		355				360						365												
GCT	AAG	GTT	TTG	GTT	GTG	ATG	CTA	CTC	TTT	GCC	GGC	GTC	GAC	GGG	CAT	1152								
Ala	Lys	Val	Leu	Val	Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly	His									
	370				375						380													
ACC	CGC	GTG	TCA	GGA	GGG	GCA	GCA	GCC	TCC	GAT	ACC	AGG	GGC	CTT	GTG	1200								
Thr	Arg	Val	Ser	Gly	Gly	Ala	Ala	Ala	Ser	Asp	Thr	Arg	Gly	Leu	Val									
	385			390					395					400										
TCC	CTC	TTT	AGC	CCC	GGG	TCG	GCT	CAG	AAA	ATC	CAG	CTC	GTA	AAC	ACC	1248								
Ser	Leu	Phe	Ser	Pro	Gly	Ser	Ala	Gln	Lys	Ile	Gln	Leu	Val	Asn	Thr									
			405					410						415										
AAC	GGC	AGT	TGG	CAC	ATC	AAC	AGG	ACT	GCC	CTG	AAC	TGC	AAC	GAC	TCC	1296								
Asn	Gly	Ser	Trp	His	Ile	Asn	Arg	Thr	Ala	Leu	Asn	Cys	Asn	Asp	Ser									
			420				425						430											

CTC	CAA	ACA	GGG	TTC	TTT	GCC	GCA	CTA	TTC	TAC	AAA	CAC	AAA	TTC	AAC	1344
Leu	Gln	Thr	Gly	Phe	Phe	Ala	Ala	Leu	Phe	Tyr	Lys	His	Lys	Phe	Asn	
	435						440					445				
TCG	TCT	GGA	TGC	CCA	GAG	CGC	TTG	GCC	AGC	TGT	CGC	TCC	ATC	GAC	AAG	1392
Ser	Ser	Gly	Cys	Pro	Glu	Arg	Leu	Ala	Ser	Cys	Arg	Ser	Ile	Asp	Lys	
	450					455					460					
TTC	GCT	CAG	GGG	TGG	GGT	CCC	CTC	ACT	TAC	ACT	GAG	CCT	AAC	AGC	TCG	1440
Phe	Ala	Gln	Gly	Trp	Gly	Pro	Leu	Thr	Tyr	Thr	Glu	Pro	Asn	Ser	Ser	
465					470					475					480	
GAC	CAG	AGG	CCC	TAC	TGC	TGG	CAC	TAC	GCG	CCT	CGA	CCG	TGT	GGT	ATT	1488
Asp	Gln	Arg	Pro	Tyr	Cys	Trp	His	Tyr	Ala	Pro	Arg	Pro	Cys	Gly	Ile	
				485					490					495		
GTA	CCC	GCG	TCT	CAG	GTG	TGC	GGT	CCA	GTG	TAT	TGC	TTC	ACC	CCG	AGC	1536
Val	Pro	Ala	Ser	Gln	Val	Cys	Gly	Pro	Val	Tyr	Cys	Phe	Thr	Pro	Ser	
			500					505					510			
CCT	GTT	GTG	GTG	GGG	ACG	ACC	GAT	CGG	TTT	GGT	GTC	CCC	ACG	TAT	AAC	1584
Pro	Val	Val	Val	Gly	Thr	Thr	Asp	Arg	Phe	Gly	Val	Pro	Thr	Tyr	Asn	
		515					520					525				
TGG	GGG	GCG	AAC	GAC	TCG	GAT	GTG	CTG	ATT	CTC	AAC	AAC	ACG	CGG	CCG	1632
Trp	Gly	Ala	Asn	Asp	Ser	Asp	Val	Leu	Ile	Leu	Asn	Asn	Thr	Arg	Pro	
	530					535					540					
GCG	CGA	GGC	AAC	TGG	TTC	GGC	TGT	ACA	TGG	ATG	AAT	GGC	ACT	GGG	TTC	1680
Pro	Arg	Gly	Asn	Trp	Phe	Gly	Cys	Thr	Trp	Met	Asn	Gly	Thr	Gly	Phe	
545					550					555					560	
ACC	AAG	ACG	TGT	GGG	GGC	CCC	CCG	TGC	AAC	ATC	GGG	GGG	GCC	GGC	AAC	1728
Thr	Lys	Thr	Cys	Gly	Gly	Pro	Pro	Cys	Asn	Ile	Gly	Gly	Ala	Gly	Asn	
				565					570					575		
AAC	ACC	TTG	ACC	TGC	CCC	ACT	GAC	TGT	TTT	CGG	AAG	CAC	CCC	GAG	GCC	1776
Asn	Thr	Leu	Thr	Cys	Pro	Thr	Asp	Cys	Phe	Arg	Lys	His	Pro	Glu	Ala	
			580					585					590			
ACC	TAC	GCC	AGA	TGC	GGT	TCT	GGG	CCC	TGG	CTG	ACA	CCT	AGG	TGT	ATG	1824
Thr	Tyr	Ala	Arg	Cys	Gly	Ser	Gly	Pro	Trp	Leu	Thr	Pro	Arg	Cys	Met	
		595					600					605				
GTT	CAT	TAC	CCA	TAT	AGG	CTC	TGG	CAC	TAC	CCC	TGC	ACT	GTC	AAC	TTC	1872
Val	His	Tyr	Pro	Tyr	Arg	Leu	Trp	His	Tyr	Pro	Cys	Thr	Val	Asn	Phe	
	610					615					620					
ACC	ATC	TTC	AAG	GTT	AGG	ATG	TAC	GTG	GGG	GGC	GTG	GAG	CAC	AGG	TTC	1920
Thr	Ile	Phe	Lys	Val	Arg	Met	Tyr	Val	Gly	Gly	Val	Glu	His	Arg	Phe	
625					630					635					640	
GAA	GCC	GCA	TGC	AAT	TGG	ACT	CGA	GGA	GAG	CGT	TGT	GAC	TTG	GAG	GAC	1968
Glu	Ala	Ala	Cys	Asn	Trp	Thr	Arg	Gly	Glu	Arg	Cys	Asp	Leu	Glu	Asp	
				645					650					655		
AGG	GAT	AGA	TCA	GAG	CTT	AGC	CCG	CTG	CTG	CTG	TCT	ACA	ACA	GAG	TGG	2016
Arg	Asp	Arg	Ser	Glu	Leu	Ser	Pro	Leu	Leu	Leu	Ser	Thr	Thr	Glu	Trp	
			660					665						670		

CAG ATA CTG CCC TGT TCC TTC ACC ACC CTG CCG GCC CTA TCC ACC GGC Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr Gly 675 680 685	2064
CTG ATC CAC CTC CAT CAG AAC ATC GTG GAC GTG CAA TAC CTG TAC GGT Leu Ile His Leu His Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr Gly 690 695 700	2112
GTA GGG TCG GCG GTT GTC TCC CTT GTC ATC AAA TGG GAG TAT GTC CTG Val Gly Ser Ala Val Val Ser Leu Val Ile Lys Trp Glu Tyr Val Leu 705 710 715 720	2160
TTG CTC TTC CTT CTC CTG GCA GAC GCG CGC ATC TGC GCC TGC TTA TGG Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu Trp 725 730 735	2208
ATG ATG CTG CTG ATA GCT CAA GCT GAG GCC GCC TTA GAG AAC CTG GTG Met Met Leu Leu Ile Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu Val 740 745 750	2256
GTC CTC AAT GCG GCG GCC GTG GCC GGG GCG CAT GGC ACT CTT TCC TTC Val Leu Asn Ala Ala Ala Val Ala Gly Ala His Gly Thr Leu Ser Phe 755 760 765	2304
GTT GTG TTC TTC TGT GCT GCC TGG TAC ATC AAG GGC AGG CTG GTC CCT Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val Pro 770 775 780	2352
GGT GCG GCA TAC GCC TTC TAT GGC GTG TGG CCG CTG CTC CTG CTT CTG Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu Leu 785 790 795 800	2400
CTG GCC TTA CCA CCA CGA GCT TAT GCC TAGTAA Leu Ala Leu Pro Pro Arg Ala Tyr Ala 805 810	2433

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 809 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn	
1				5					10					15		
Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly	Gln	Ile	Val	Gly	
			20					25					30			
Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro	Arg	Leu	Gly	Val	Arg	Ala	
			35				40					45				
Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	
			50			55					60					
Ile	Pro	Lys	Ala	Arg	Arg	Pro	Glu	Gly	Arg	Ala	Trp	Ala	Gln	Pro	Gly	
65				70				75						80		

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp  
85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro  
100 105 110

Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys  
115 120 125

Gly Phe Ala Asp Leu Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu  
130 135 140

Gly Gly Ala Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp  
145 150 155 160

Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile  
165 170 175

Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr  
180 185 190

Glu Val Arg Asn Val Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser  
195 200 205

Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro  
210 215 220

Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val  
225 230 235 240

Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr  
245 250 255

Thr Ile Arg Arg His Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys  
260 265 270

Ser Ala Met Tyr Val Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser  
275 280 285

Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys  
290 295 300

Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met Ala Trp  
305 310 315 320

Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val Val Ser Gln  
325 330 335

Leu Leu Arg Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His  
340 345 350

Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp  
355 360 365

Ala Lys Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His  
370 375 380

Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val  
385 390 395 400

Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr  
 405 410 415  
 Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser  
 420 425 430  
 Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn  
 435 440 445  
 Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys  
 450 455 460  
 Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser  
 465 470 475 480  
 Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile  
 485 490 495  
 Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser  
 500 505 510  
 Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn  
 515 520 525  
 Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro  
 530 535 540  
 Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe  
 545 550 555 560  
 Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn  
 565 570 575  
 Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala  
 580 585 590  
 Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met  
 595 600 605  
 Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe  
 610 615 620  
 Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe  
 625 630 635 640  
 Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp  
 645 650 655  
 Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu Trp  
 660 665 670  
 Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr Gly  
 675 680 685  
 Leu Ile His Leu His Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr Gly  
 690 695 700  
 Val Gly Ser Ala Val Val Ser Leu Val Ile Lys Trp Glu Tyr Val Leu  
 705 710 715 720  
 Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu Trp

[illegible]

(2) INFORMATION FOR SEQ ID NO: 51:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- ```
(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 1..17
```

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

Ser Asn Ser Ser Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys  
1 5 10 15  
Val

(2) INFORMATION FOR SEQ ID NO: 52:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- ```
(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 1..22
```

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Gly Gly Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp

1                      5                      10                      15

Ser Pro Thr Thr Ala Leu  
20

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..37

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

Tyr Glu Val Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp Cys  
1                      5                      10                      15  
Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met His Thr  
20                      25                      30  
Pro Gly Cys Gly Lys  
35

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Gly Gly Thr Pro Thr Val Ala Thr Arg Asp Gly Lys Leu Pro Ala Thr  
1                      5                      10                      15  
Gln Leu Arg Arg His Ile Asp Leu Leu  
20                      25

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid

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(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 1..25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

Gly Gly Thr Pro Thr Leu Ala Ala Arg Asp Ala Ser Val Pro Thr Thr  
1 5 10 15  
Thr Ile Arg Arg His Val Asp Leu Leu  
20 25

00073025-101001

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Gln Val Arg Asn  
1 5 10 15  
Ser Thr Gly Leu  
20

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

Gln Val Arg Asn Ser Thr Gly Leu Tyr His Val Thr Asn Asp Cys Pro  
1 5 10 15  
Asn Ser Ser Ile  
20

(2) INFORMATION FOR SEQ ID NO: 58:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

Asn Asp Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala His Asp Ala Ile  
 1                      5                      10                      15  
 Leu His Thr Pro  
                     20

(2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met His Thr  
 1                      5                      10                      15  
 Pro Gly Cys Val  
                     20

(2) INFORMATION FOR SEQ ID NO: 60:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 19 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

His Asp Ala Ile Leu His Thr Pro Gly Val Pro Cys Val Arg Glu Gly  
 1                      5                      10                      15  
 Asn Val Ser

(2) INFORMATION FOR SEQ ID NO: 61:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

Cys Val Arg Glu Gly Asn Val Ser Arg Cys Trp Val Ala Met Thr Pro  
1                      5                      10                      15

Thr Val Ala Thr  
20

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

Ala Met Thr Pro Thr Val Ala Thr Arg Asp Gly Lys Leu Pro Ala Thr  
1                      5                      10                      15

Gln Leu Arg Arg  
20

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

Leu Pro Ala Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val Gly Ser  
1                      5                      10                      15

Ala Thr Leu Cys  
20

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

Leu Val Gly Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu  
1                      5                      10                      15  
Cys Gly Ser Val  
                    20

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

Gln Leu Phe Thr Phe Ser Pro Arg Arg His Trp Thr Thr Gln Gly Cys  
1                      5                      10                      15  
Asn Cys Ser Ile  
                    20

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

Thr Gln Gly Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His  
1                      5                      10                      15  
Arg Met Ala Trp  
                    20

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser Pro  
1 5 10 15  
Thr Ala Ala Leu  
20

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

Asn Trp Ser Pro Thr Ala Ala Leu Val Met Ala Gln Leu Leu Arg Ile  
1 5 10 15  
Pro Gln Ala Ile  
20

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

Leu Leu Arg Ile Pro Gln Ala Ile Leu Asp Met Ile Ala Gly Ala His  
1 5 10 15  
Trp Gly Val Leu  
20

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

Ala Gly Ala His Trp Gly Val Leu Ala Gly Ile Ala Tyr Phe Ser Met  
1 5 10 15  
Val Gly Asn Met  
20

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

Val Val Leu Leu Leu Phe Ala Gly Val Asp Ala Glu Thr Ile Val Ser  
1 5 10 15  
Gly Gly Gln Ala  
20

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

Ser Gly Leu Val Ser Leu Phe Thr Pro Gly Ala Lys Gln Asn Ile Gln  
1 5 10 15  
Leu Ile Asn Thr  
20

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

Gln Asn Ile Gln Leu Ile Asn Thr Asn Gly Gln Trp His Ile Asn Ser  
1 5 10 15  
Thr Ala Leu Asn  
20

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

Leu Asn Cys Asn Glu Ser Leu Asn Thr Gly Trp Trp Leu Ala Gly Leu  
1 5 10 15  
Ile Tyr Gln His Lys  
20

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

Ala Gly Leu Ile Tyr Gln His Lys Phe Asn Ser Ser Gly Cys Pro Glu  
1 5 10 15  
Arg Leu Ala Ser  
20

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Pro Leu Thr Asp Phe Asp  
1 5 10 15  
Gln Gly Trp Gly  
20

(2) INFORMATION FOR SEQ ID NO: 77:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

Thr Asp Phe Asp Gln Gly Trp Gly Pro Ile Ser Tyr Ala Asn Gly Ser  
1 5 10 15  
Gly Pro Asp Gln  
20

(2) INFORMATION FOR SEQ ID NO: 78:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

Ala Asn Gly Ser Gly Pro Asp Gln Arg Pro Tyr Cys Trp His Tyr Pro  
1 5 10 15  
Pro Lys Pro Cys  
20

(2) INFORMATION FOR SEQ ID NO: 79:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

09973025-101001



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

Trp His Tyr Pro Pro Lys Pro Cys Gly Ile Val Pro Ala Lys Ser Val  
1 5 10 15  
Cys Gly Pro Val  
20

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

Ala Lys Ser Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val  
1 5 10 15  
Val Val Gly Thr  
20

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Ser Gly Ala Pro Thr  
1 5 10 15  
Tyr Ser Trp Gly  
20

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

00973025-100001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

Gly Ala Pro Thr Tyr Ser Trp Gly Glu Asn Asp Thr Asp Val Phe Val  
1 5 10 15

Leu Asn Asn Thr  
20

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Ser Thr Gly Phe Thr Lys  
1 5 10 15

Val Cys Gly Ala  
20

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

Gly Phe Thr Lys Val Cys Gly Ala Pro Pro Val Cys Ile Gly Gly Ala  
1 5 10 15

Gly Asn Asn Thr  
20

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

00973025-01001

Ile Gly Gly Ala Gly Asn Asn Thr Leu His Cys Pro Thr Asp Cys Arg  
 1 5 10 15

Lys His Pro

(2) INFORMATION FOR SEQ ID NO: 86:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

Thr Asp Cys Phe Arg Lys His Pro Asp Ala Thr Tyr Ser Arg Cys Gly  
 1 5 10 15

Ser Gly Pro Trp  
 20

(2) INFORMATION FOR SEQ ID NO: 87:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

Ser Arg Cys Gly Ser Gly Pro Trp Ile Thr Pro Arg Cys Leu Val Asp  
 1 5 10 15

Tyr Pro Tyr Arg  
 20

(2) INFORMATION FOR SEQ ID NO: 88:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

Cys Leu Val Asp Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Ile

09973025401001

1                      5                      10                      15

Asn Tyr Thr Ile  
20

(2) INFORMATION FOR SEQ ID NO: 89:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

Pro Cys Thr Ile Asn Tyr Thr Ile Phe Lys Ile Arg Met Tyr Val Gly  
1                      5                      10                      15

Gly Val Glu His  
20

(2) INFORMATION FOR SEQ ID NO: 90:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

Met Tyr Val Gly Gly Val Glu His Arg Leu Glu Ala Ala Cys Asn Trp  
1                      5                      10                      15

Thr Pro Gly Glu  
20

(2) INFORMATION FOR SEQ ID NO: 91:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

Ala Cys Asn Trp Thr Pro Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp  
1                      5                      10                      15

Arg Ser Glu Leu  
20

(2) INFORMATION FOR SEQ ID NO: 92:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu Thr Thr Thr  
1 5 10 15  
Gln Trp Gln Val  
20

(2) INFORMATION FOR SEQ ID NO: 93:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

Tyr Gln Val Arg Asn Ser Thr Gly Leu  
1 5

(2) INFORMATION FOR SEQ ID NO: 94:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

ACGTCCGTAC GTTCGAATTA ATTAATCGA

(2) INFORMATION FOR SEQ ID NO: 95:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 60 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

00973025-101001 CCTCCGGACG TGCACTAGCT CCCGTCTGTG GTAGTGGTGG TAGTGATTAT CAATTAATTG 60

(2) INFORMATION FOR SEQ ID NO: 96:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 19 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

GTTTAACCAC TGCATGATG 19

(2) INFORMATION FOR SEQ ID NO: 97:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

GTCCCATCGA GTGCGGCTAC

20

(2) INFORMATION FOR SEQ ID NO: 98:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 45 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

GGTGACATGG TACATTCCGG ACACTTGGCG CACTTCATAA GCGGA

45

(2) INFORMATION FOR SEQ ID NO: 99:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 42 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

TGCCTCATAC ACAATGGAGC TCTGGGACGA GTCGTTCTGTG AC

42

(2) INFORMATION FOR SEQ ID NO: 100:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 42 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

TACCCAGCAG CGGGAGCTCT GTTGCTCCCG AACGCAGGGC AC

42

(2) INFORMATION FOR SEQ ID NO: 101:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 42 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

TGTCGTGGTG GGGACGGAGG CCTGCCTAGC TGCGAGCGTG GG

42

(2) INFORMATION FOR SEQ ID NO: 102:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 48 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

CGTTATGTGG CCCGGGTAGA TTGAGCACTG GCAGTCCTGC ACCGTCTC

48

(2) INFORMATION FOR SEQ ID NO: 103:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 42 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

CAGGGCCGTT CTAGGCCTCC ACTGCATCAT CATATCCCAA GC

42



(2) INFORMATION FOR SEQ ID NO: 104:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

CCGGAATGTA CCATGTCACG AACGAC

26

(2) INFORMATION FOR SEQ ID NO: 105:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

GCTCCATTGT GTATGAGGCA GCGG

24

(2) INFORMATION FOR SEQ ID NO: 106:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

GAGCTCCCGC TGCTGGGTAG CGC

23

(2) INFORMATION FOR SEQ ID NO: 107:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 25 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO  
(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

CCTCCGTCCC CACCACGACA ATACG

25

(2) INFORMATION FOR SEQ ID NO: 108:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 27 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO  
(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

CTACCCGGGC CACATAACGG GTCACCG

27

(2) INFORMATION FOR SEQ ID NO: 109:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 24 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO  
(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

GGAGGCCTAC AACGGCCCTG GTGG

24

(2) INFORMATION FOR SEQ ID NO: 110:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 22 base pairs

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

TTCTATCGAT TAAATAGAAT TC

22

(2) INFORMATION FOR SEQ ID NO: 111:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

GCCATACGCT CACAGCCGAT CCC

23

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